

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCAGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTC
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG
CTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATGCCCCCTGCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCCTCCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCTCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAA
CGTGAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCVPGGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCAGAGTCCCCCTCGCGGCAGCAGATGTGTGTGGG
 GTCAGCCACCGCGGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCCTGATC
 CGGTTCTTGGTGCCCCCTGGGCATACCAACATAGCCATCGACTTCGGGGAGCAGGCCCTTGAA
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
 ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGAAGTTCAAAAATGTGGGCCTGGTGT
 GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC
 TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
 ACCATGTGGACGAGTCCGTGGGGAGCAAGACGAGAAGGGCCTTCTGTACCTCGCCGCCTTT
 CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
 CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC
 TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC
 GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACAGACATCATCCC
 TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
 GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
 TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
 CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG
 ACAAGAATAACCCCAGCAACAACTGGTGAGCAGCAGCAACACAGTCACGGCAGCCACATC
 AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
 ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTCGAGAAC
 TCTGTGTGTTCTTTTGCAGATCTTCTCCTTCTTCCAGTTCCAGTCACAGTGAGGGCGCAT
 CTCACCGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTGCG
 GATCATCGTCTCATCGCCAGCCTCGTGGTCTTACCCTACCTGGGGGTGCACGGTGCAGCCC
 TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTGCCTATCGCTGCG
 TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA
 CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG
 AGAATGAATAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
 GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTGTTTTGTTTGGTAAT
 GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
 GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC
 TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC
 TCCTCCCCTGGACAATCTCCTCTTGGAAACCAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
 CACCCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
 TTAAAACTCGGCTTCTTTTGTGTTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
 CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
 GAGGCGGGTGGCAGCTGCAGCCCGGAGTCCCCGTTACACTGAGGAACGGAGACCTGTGAC
 CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG
 GGCAGCAAACCTGACATGGTTGAATGATAGCATTTCCTCTGCGTTCTCCTAGATCTGAGCAA
 GCTGTGAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCACAAA
 GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC
 CTTTCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT
 TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTTCTAATGCCAGGTTGCTGTAGGGTAAC
 TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA
 TTGAGAATGTACTACGGTACTTCCCTCCCACACCATAACGATAAAGCAAGACATTTTATAACG
 ATACCAGAGTCACATATGTGGTCTCCTGAAATAACGCATTCGAAATCCATGCAGTGCAGTA
 TATTTTTCTAAGTTTTTGGAAAGCAGGTTTTTCTTTAAAAAAATATATAGACACGGTTCACT
 AAATTGATTTAGTCAGAAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
 TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCGC
 ATTTTCAATAAAATGTCTCTAATACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSTDFKNVGLVFNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIINKLHHVDESV
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLC LGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVVPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVBHGATLGVGSL
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEEVTDIVEMRENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

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[illegible][illegible]

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTTCCTTTGCGGATTTTCT
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

604006: 98024001

FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTTCCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACTGAGCCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCCTGCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT
GGCCTCACTGCACGTCATGATGACGCTACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACT
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCCTCCTCCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTTGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAAACAAGCCAGTGCGTGTAACAAAAA

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE
SOLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLFILIQLVLLIDFAHSW
NQRWLKGAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVITYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAGGCCATGGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG
TGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGG
TGTATGGGGGAATAACCAGCTTTTATTATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGTATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA
GCTGTCACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGCCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTACGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTTCTTTTCTT
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAETIYHNRFDVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGTCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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Figure 1 consists of 12 panels (a-l) showing Western blot analysis of protein expression in 293T cells. Each panel has lanes for 'Control' and 'Protein' (with increasing concentrations of the indicated protein). Molecular weight markers are shown on the left of each panel. The panels are: (a) p53, (b) p21, (c) p27, (d) p107, (e) p130, (f) p15, (g) p16, (h) p18, (i) p19, (j) p20, (k) p21, (l) p27. The blots show that the expression of the indicated protein increases with concentration, leading to the upregulation of downstream targets like p21 and p27.

GAGCCGCGCCGCGCGCGCCGCGCACTGCAGGCCAGGCCCGGCCCCACCACCGTCT
GCGTTGCTGCCCCGCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCGGGG
GCTTCGCGTGTTCGAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTTCTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTTATT
GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
TGGCATTGGCCTGTTCTTCAGTTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCATTCTTTTGAATGAGAAAACAAGGAAGAT
TTCCTTTCGTATTATGATCTTGTTCACTTTCTGTAATTTCTGTTAAGCTCCATTTGCCAGT
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCATTGTCGGGCACTGTCCACTGTGGCCTT
TCTTAGCATTTTTTACCTGCAGAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCTCTAC
TGGAAAAAGAGTGGAATTTATTAAAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATTCCTCAATTTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATTGTGGTTTAAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
AAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTCAGCAAAAAGATATTTG
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT
GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA
ATTAAAAAGAAAGTAATGGAAG

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVGVVIAVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFVGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT
TGTATTTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

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FIGURE 17

AATCCCAAATTCCCAATTTTTTTTGGNCTTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
 TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
 TTATGTCTTAGGAAATTGTGGTTTAATTTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
 GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
 AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
 TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
 ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
 AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
 GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
 CCACTTGC

[illegible][illegible]

FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCCTCCACCTGATTGTGTCCTATGACTGGCTG
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTTGGGATCCAGAAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGA
GGAGGCCCTTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTTCATCCATGATCTCACT
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGTCCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCCAGTGTTTTGTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCACAAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATAACAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTTCTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG
ACTCTGTCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG
TTGTTTGTAGCCTAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSAAPPPTLNPAQKSAAPGTAPEEAPGPLPPPPTPSSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTTTGACCCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAGTGTCTGTATAAAATGCCCCATTAGGC
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

protein = seqdb2

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTGCGGA
GGCGCCCGGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
GGGATGTCCTCCTCCTTCTCCTTCTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCTGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAACGTGTACAGT
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCTCCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCTCCACTCGCTCCACAGCAAAT
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACACACCCAGCATGATCCCAGCCAGAGCAGAGCCTTCCAA
ACGGTCTGAATTACAATGGACTTGACTCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTTCTTATACAATAACCAAACAAGCAAA
AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAATT
TTCAAGAGGAAATGGGATGCTGTTTGTAATTTCTATGCATTTCTGCAAACTTATTGGATT
ATTAGTTATTGAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTGATCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCCTCAAAT
CAGATGCCTCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT
TATCAACGTCTTAGAAAGAAATTTCTTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA
CCCAACATACCATATAGTCTCTTCTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

[illegible]

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><subunit 1 of 1, 373 aa, 1 stop
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><MW: 41281, pI: 8.33, NX(S/T): 3

Signal sequence:

Transmembrane domain:

amino acids 232-251

FIGURE 25

GTCGTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
GACGCGGGCTGCAATCGCGCGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCGAGTGTGAGCGCCCCTAG
AGCCTCCCTTGCCGCTCCTCCTCTGCCCCGCGCAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCC
GCCGGGAGGCGCGGTGGATGCGGCGCTGGGCAGAGCAGCCGCGATTCCAGCTGCCCCGCGCCCCGGCG
CCCCGCGAGTCCCCGTTTCAAGGACCTCTCCGAGCAGCAGCACCCGCTCGCCTCCTGCAGCCGCATC
GCCCCGCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCTGCTTGGATTCTTAGCACCACCACAGCTCAG
CCAGAACAGAAGGCCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAAGCATGCCATGGCCAATG
ATTGAGAAATTACCTTGTGTGCTTGTACTGACCGAGAATGCACCTTGCCACCTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCCCATACCGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
CTGAGTCAGAACCTGGTGGTGTATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTTTC
TCCAGCTCCACCTCACCTTCCCCCTGGCACAGCCATCTTCCACGCTGAGCACATGGAAACCCATGAAGTCCCT
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTTCTGCTCTGTTAGACCAAAGGTACTG
AGTAGACTCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
CATTTTGACATCAATGAGCATTGTGCTTGGATGATTGTGCTTTTCTGCTGCTGGTGTCTGTGGTGTATTGTGGT
TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAGGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
AGGGAGGTGTGCTTCTCCAATGGGTACACAGCCGACCACGAGCGGCTTACGAGCTCTGCAGCACTGGACC
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG
AAGATTGCTGGGTGTGGAAGACACCCAGCTGGAAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG
CTTAGCCCCAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTCCGCTCTCTGACGGTGGAGCCTTCCCCA
CAGGACAAGAACAAGGGCTTCTCGTGGATGAGTCGGAGCCCCCTCTCGCTGTGACTCTACATCCAGCGGCTCC
TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAAGAAAAGAGGACACAGTGTGCGGCAGGTACGCCCTGGAC
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGTATGAAGAG
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGCAAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAATTACTCA
ATTTAGTGGCAGGGTGGTTTTTAATTTTCTTCTGTTTCTGATTTTGTGTTTGGGGTGTGTGTGTGTGTGTGT
GT
TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA
ATACCCACCACTAAAGTTTTTAAAGTTCCATATTTTCTCCATTTTGCCTTCTTATGTATTTTCAAGATTATTCTG
TGCACTTTAAATTTACTTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTATGTCTCTTAACATTACACCTACTTTTT
AAAAACAAATATTATTACTATTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGA
CCCCATTGAGTTACTGTAAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTGTATAGTTTCATATTTCATGG
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCCTGGACACCGTGTAGAATGCTTGATTACTTGTAC
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
GACAACCTGGGCCACCAAGAACTTGAACCTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACCTT
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
TTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGCTGGTGGGATTCTTCCCAATT
ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTGCAACTATGCTCCCAATTACAAATG
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA
AAAAA

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCS SCPVGTFRHENGIEKCHDCSQPCPWPMIEKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPLNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVA AQVGSQWKDIY
QFLCNASEREVA AFSNGYTADHERAYAALQHW TIRGPEASLAQLISALRQHRNDVVEKIRG
LMEDTTQLETDKLALPMSPLSPSPPIPSNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALS RNGSFITKEKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCC
TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAAATGCCGTGCTCCAGGTGTTTACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC
TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCT
GTGGTATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTCTATCAC
GCCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCGTGCTCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTCACCTCCTTCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCCGGCACCA
GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCCGCCACCACACCCAACTAATTTTTGTATTTTTAGTAGAGAC
AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCCACAGTGTGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC
TGATCTTCACTAAGAACAAGAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC
ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAAACCCACCTTTCTACTTCCAAGACTTAT
TTTACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT
TGTAGCATTTGGTGCTTGACGTATTATTTGTCTTTGATTCCAAATAATATGTTTTCTTCCCT
CATTTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLOVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKV TALHH
SVYVREGCASGHVVT LQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIIITAAHC VYDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMI QPVCLPNSEENFPD GKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHR
DVG GGIISPSMLCAGYLTGGVDSCQGD SGGPLVCQERRLWKLVGATSFGIGCAEVNKP G VYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

protein sequence

[illegible]

CCACGCGTCCGTCTCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTATTATGCAAGCGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCACGCACGCACACACGCGGGGAAACTTTTTTAAAAAATGAAAGGCTAGAGA
GCTCAGCGCGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTGC
CGCCCGGCCCCGGCTCGGCGCCCCGCTGGGATGGTGCAGCGCTCGCCGCCGGGCCCCGAGAGCTGCTGCACTGAAG
GCCGGCGACGATGGCAGCGCGCCCCGCTGCCCCGTGTCCCCCGCCCGCGCCCTCCTGCTCGCCCTGGCCGGTGTCTCT
GCTCGGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCTAGTGCCTCTGT
TCGGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTCGACT
ACAACGGGAAAGCAAGAAGTATGATATAAATCTGGAAGAAATGAAGGCTCATTTGCCAGCAGTTTCACGGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
ACGGGGATATTCTGATTAGCAGTCACTCTCAGCACGTGTTCTGGTCTCAGGGGACTTTATTGTGTTTGAATAATGA
AAGCTATGTCTTAGAACCAATGAAAAGTGAACCAACAGATACAACTCTTCCAGCGAAGAAGCTGAAAAGCGT
CCGGGGATCATGTGGATACATCACAAACACCAAACTCGCTGCAAAGAATGTGTTTCCACCACCCTCTCAGAC
ATGGGCAAGAAGGCATAAAAGAGAGACCTCAAGGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG
AGAGTTTCAGAGGCAGGAAAAGATCTGAAAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA
GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAAGTGTGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAATCCCA
TGACAATGCGCAGCTTGTCTAGTGGGGTTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG
CACGGCAGACCACTGTGGGGGAATTGTCTAGGACCATTGAGACAATCCCTTGGTGCAGCCGTGACCTTGGCACA
TGAGCTGGGCCCCAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
AGAGGCTGCATCATGAACGCTTCCACCGGGTACCATTTCCTATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTTTTAACCTGCCGAAGTCAAGGAGTCTTTCCGGGGCCA
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGAGCCAGGAATGTATGAATCGCTG
CTGCAATGCCACCACCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGCCAGCCC
TCACTGCCCAGCCAATGTGTACCTGACAGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCAGCAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
GAGAGTCAATTCGCAAGGTGATCCTTTATGCGCACTGTGGCAAAGTCTCGAAGAGTTCTTTTGCCAAATGCGGAT
GAGAGATGCTAAATGTGGAATAATCCAGTGTCAAGGAGGTGCCAGCCAGTCAGTCAATGGTACCAATGCCGTTT
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGACCCAGCTGTACTTGGGCGATGA
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGGTTTACGAGTGTGCAATGCAGTGCCACGCGCAGAGGGGTGTGCAACACAGGAAGAA
CTGCCACTGCGAGGCCCTTGGGCACTTCCCTTCTGTGACAAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCCC
CTCCGGCAAGCAGCAAGCAGGAGGAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCAGGAGCCCGTGGG
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACATCACTCTGAGCCCTCCCATGACATGGAGACCGTGACCAGTG
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCCTCCTGTGACTGGCAGCATTTGACTCTGTGGCTTTGCCATCGTT
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
CAGTGCACAGGAAGGGCAGCGACTTCCCTGTTGAGCTTCTGCTAAAAATGGACATGCTTCAGTGTCTGCTCCTGAG
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAGTCTGGCCTTTT
ACTGAGCCTCCACAGCAGTGTGGGGGAGAGCAAGGTTTGGGCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCAATTTATTATGAAAAT
AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCTTGCCACCCATTCCATCTCCATCCAAGCAAATGAATGGCAA
TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC
AGTACTCAGTCTTGAGGGTTTGCAAGAACCCAGGGAAACCCACAGAGTCAACAACCTTCATTTAACAAGTAAGAA
GTTTAAAAAAGTGAAAAAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVVSASVRSGLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPFPPSQTWARRHKRETLCATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWVNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFQQKCGNRFVEEGEE
CDCGEPEECMNRCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGDCYNGICQTHEQQCVTLWGPAGKAPAGICFERVNSAGDPYGN
CGKVSKESSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLOQGGRIICRGTHVYLG
DDMPDPGLVLGATKCADGKICLNRCQCNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDGPIRQAEARQEAESNRERGQGEFVGSQEHASTASLTLL

Signal peptide:

amino acids 1-28

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FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCAGTGAAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCGCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT
GAAACCATAACCTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAACAAAAAATTTGCATCACTTTTAAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTCGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTGTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCTACTTGCTATCTCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCGTGACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCACTGGCT
CACGCCTGTAATCCCGGCACCTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTGCACTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

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FIGURE 34

CCCCGCGCGAGAGCGCGCCCCAGCCCCGCGCGATGCCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGGCGGCGCTGGGGCGCCCCGGGCCAGG
AGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGACGCGGAGGACGGACAGGACCCGCACAGCAAGCACC
TGTACACGGCCGACATGTTACGCGACGGGATCCAGAGCGCCGCGCACTTCGTTCATGTTCTTCGCGCCCTGGTGTG
GACACTGCCAGCGGCTGCAGCCGACTTGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCAGGATACCCACCTTAA
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCAGACACTGGAAAACTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCAGTGCCCCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCAGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCCTTGAACATTCGGAACCTG
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGGAACACAGGTTCTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAGCGGGATTTGGAGTCACTGAGGGAGTACG
TGGAGTCGCAGCTGCAGCGCACAGAGACTGAGCGGACGAGACCGTCACGCCCTCAGAGGCCCCCGGTGCTGGCAG
CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCTACTTGGGAGGAACCTCTCTA
AAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTCAC
CTCTCCTGCCAGCTCCCCGACCCCTGCTTTAGGAGTTCACTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
GTTCAAGAACGAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTTTCAAGCCAACACACTCTACAG
ATCTTTTATTAAGTTAAGTTTCTTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTCAGTGGCGATA
TATCCCCCTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC
CCACGAGTTCTGGAAGGTGGCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAATAC
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGCGCGCTGC
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
GTGCCCTGAGTAAGAGAATGCTGATGCCATACTTTATGTGTGATACCTTGTCAAATCAGTTACTGTTTCAGGGGAT
CCTTCTGTTTCTCACGGGGTGAACCATGTCTTTAGTTCTCATGTTAACACGAAGCCAGAGCCACATGAACTGT
TGGATGTCTTCTTAGAAAGGGTAGGCATGGAATTTCCACGAGGCTCATTCTCAGTATCTCATTAACCTCATTGA
AAGATTCCAGTTGTATTTGTCACTTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCCTGGGTATCCAGGGAGGC
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGCATCCAACACTCTTCACCCACCT
CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCCTTAAAGGAAATCTTTATTAATCAG
TATGGTTCACAGATAATTCTTTTTTAAAAAAACCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
CACAACCTCAGCTTTGCATCAGAGTCTTGATTCCAAGAAAATCAAAGTGTACAATTTGTTTGTTTACACTAT
GATACTTTCTAAATAAACTCTTTTTTTTTTAA

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLNWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFEHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

FIGURE 36

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCCTTGAATACCTGGAGAAAAAGGCAAAGCAGGTA
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAAAAA

[illegible]

amino acids 1-25

FIGURE 38

GGTTCATATCGATTTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCCTGTGGAGTGGTGGGGGCCTGGGTGGGAATGGGCGTGT
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCGCCGCGC
ACACCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT
CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
GTTTCGGGCTGGCCAAGGCCGCTGCGCACTGCCTTTGTGCCACCCGCCCTGCGCCGGGGCC
CCCTGCTGCACTGCCTCCGCACTGCGGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG
GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC
ACCTCTGGCACCACGGGCCTCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC
TCTACCACATGTCCGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAG
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCGGGCCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGC
ATATCTTCCCCCTTCTCCTTGATTGCTATGATGTCAACCAGGAGAGCCAATTCGGGACCCC
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGAGAATGTGGC
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
TTCGGATGGCAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCCTACCTGCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGG
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTGACCTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCCAACTTGTTTTATTGCAG

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQRTRAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL
LLLKLHLWPQLRWLPADLAFVAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRRFSSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGVPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGORGAVGRASW
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQ GK
LLKDVFVRPGDVFFNTGDLVCDQGF LRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLP PYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATAACACTCGCTCTC
GCTTGTCATCTCCCTCCCGGGGAGCCGGCGCGCTCCACCTTTGCCGCACACTCCGGC
GAGCCGAGCCCCGAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTTTTAAACACTTCTTTTCTTCTCTTCTCGTTTTGATTGCACCGTTTCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT
CCATCTGGCTTATAAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG
CTGGCAGAAGGGGGTGACGCTGGGCAGCGCGGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG
TTGCACCATGCCTTCTTGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC
AAGGGATTGAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
CATAAGAAATTTGACGAATTTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTGAGAAGTCTTCCAGGACCTCT
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC
GGAAACTGAAGATTGAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTGAGCCCAACCCAGGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATAGTGTGCGGGGCTTCCCACTGTGAGGCCCTGCA
ACAATACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGTCTGCAAAGGTCTTTGAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC
CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTTTGTACCA
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATA
ATCTTGGGTTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG
CTTCCCTCTTTCCTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT
CTCACGTTGTGAGGGTTTTTTTTTTCTCATTTAAAT

[illegible]

```
><subunit 1 of 1, 555 aa, 1 stop
```

MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCTT MEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELL ENAEKSLNDMF
VRTYGM LYMQNSEVFQDLFT ELKRYT TGGNVNLEEMLNDFWARLLERMFQLINPQYHFSE DY
LECVSKYTDQLKPF GDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNL FIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVS AKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDES VTAGTSNEEECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMMDDVCPTEFEFVTT EAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:
amino acids 1-23

[illegible]

CGGACGCGTGGGCGGACGCGCTGTGGGCAAAAGAACTCGGAGTGCACAAAGCTAAATAAGTTAGCTGAGAAAACGACGAC
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
TAGGGACCCGGCTTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCCCGCTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGGAAAAATAGCCCTGGGAAAGTGAGAAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA
TCCCGCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA
AAAGTTCCCTGTCCACTGTGATTCTCAATTCTTGCTTGGTTTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA
ACTTTTTTCTTTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGGCTGTGCGGGGCATCCGCCCTCCGCCCTTCTCCACAGGCCTGTGTCTGTCCTGGAAAGATGCTAGCAATGGGGG
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGCGGGCCAGGCCTTAGAAGAGGAGG
AAGAAGGGGCCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCGACACAACCTTCCACCTCCCAGCCCCATCTCA
TTTTCATCTTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTA AAAACACCTACTCTTG
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCCACTGTTTTAC
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCACGCATATGGTCGGAAAATGGCACT
TGGGTTTTTAACAGAAAAGAAATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG
GGGATTACTATACACACTACAATGTGACAGTCCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCAT
ACCCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTCATTCACCACTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAACCTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTTCGCTCACCCCGAGTAGATATTTTGATAACATTGACCCCTATACACCAAGGC
AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTTTCAGCAACCTGGGACCGAACCG
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCTACGGAGGCTCTCACAGTTCAACAAAAC
TGCAGTGCCGGTCAGGTATCCCCCAAGACCCCAAGTAACCTTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAAACCAAGAAAAAGAAGCCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAAAC
GAAGAAGAAACAGCAGAAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAACCTGTCTGTCTCAGTG
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTATTTCTCTCGCTCCTTTAGAAAACGTG
GTGAGTCTTGAGTTCCTACTGCTGTGCTTCAGTCAACTGACCAAACACTGCTTTGAATTATAGGAGGAGAAACAATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTA AAAACTACCTTTGATAAATTAC

[illegible][illegible]

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHYGSEIKTPTLDKLA AEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHVMVGKWHLGFNKKEC
MPTRRGFDFTFFGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTORVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVFVHSPLLKNKGTVCCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGGAGAATGCTCTGCCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTGAGCCT
GGGTCTGTCACTATGGAACATAAAGTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA
TTGGTTTTGCAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAAGACCCACCAGGACTCC
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAT
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGTACAAGAAAGACATTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAATTGAGTTGTATCAAGGAACTGATGC
TACCAAAGCATCATTTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCCTGGTTTTTTTGTATTTGCATCATAG
GACCTCTGGCATTTTGAATTAAGTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATG
TAAGATGCCTTTCTTGATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGAAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCCTTTGTAATAATAA

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPKNKRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSKYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

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FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGCTGTGCTCAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC
TTTAAGACAAAACATTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAATAATAAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

CGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCAGTGAAGCCTCA
ACCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCTCACTGCTGCCCAGTCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
CAGTGGTCTTGGGTTCTCTGCAGCGTGAAGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACCAGCT
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTG
GGGTGCAGGGCCCCCTGTGAGGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
CACTGGGTTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
GCTGCTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG
CTGCCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
TGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG
CATGAGGTGAGGGGCACATGGTTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCAGGCTGAGCCTGGAAGCTGCCTGGCC
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCAAATGGCATTACTGCCCCTGTCTCCCCACCCCTGTGATGTGTGATTCCAGGCAC
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC
AGGCGTCTCAGCTTTCTCTCCTTTTACTCTTTTCAATACAATCACGCCAGCCACGTTGTTT
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTAACTTAAATAAATTGTTAC
AAAATAAAA

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHVWQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTPVPTLLGPRACSRLLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGGCCCCATTGCGGGCCGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG
CCCAGCTGTCAGCCGCCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTGAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGCAGATGGCCAACGA
GCAGGGCTTGTGTTGATGTGCACAGCGTCCTGCGGGTGGTGTGCTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGG
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCTGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGA
CTGACTGACCCCTGCCTTATTTTACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTTACGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTT
CCCTCCTTCTCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCACCACCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC
TTGCCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAAC TTGTCTGAAGCCCTTGTCCGTAAGCCTTGAAC TACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACCTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATT CATCTGCCATCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTTGGTTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCCTGC
TCTGGGCTATGAAAAGAAGGAAAAGGTAAAATCCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTTTATACAATGTTCTTTCTTGCTTTGTTTTTTATTTTTTATATATTTTTT
CTGACTCCTATTTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTGAGACAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTTATGTGTGAGTTTCTTTGTAATAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCTGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPEPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGS
FHSTHKHNNQPIWFTLGILEALKGWDQGLKGMVCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLAIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

Year	Age	Sex	Location	Occupation	Education	Income	Health	Family	Community	Environment	Policy	Program	Impact	Notes
2000	25	Male	Urban	Teacher	High School	\$15,000	Good	2 children	Active	Green	Yes	Yes	10%	Initial baseline
2005	30	Male	Urban	Teacher	High School	\$18,000	Good	2 children	Active	Green	Yes	Yes	15%	Follow-up 1
2010	35	Male	Urban	Teacher	High School	\$20,000	Good	2 children	Active	Green	Yes	Yes	20%	Follow-up 2
2015	40	Male	Urban	Teacher	High School	\$22,000	Good	2 children	Active	Green	Yes	Yes	25%	Follow-up 3
2020	45	Male	Urban	Teacher	High School	\$25,000	Good	2 children	Active	Green	Yes	Yes	30%	Follow-up 4
2025	50	Male	Urban	Teacher	High School	\$28,000	Good	2 children	Active	Green	Yes	Yes	35%	Follow-up 5
2030	55	Male	Urban	Teacher	High School	\$30,000	Good	2 children	Active	Green	Yes	Yes	40%	Follow-up 6
2035	60	Male	Urban	Teacher	High School	\$32,000	Good	2 children	Active	Green	Yes	Yes	45%	Follow-up 7
2040	65	Male	Urban	Teacher	High School	\$35,000	Good	2 children	Active	Green	Yes	Yes	50%	Follow-up 8
2045	70	Male	Urban	Teacher	High School	\$38,000	Good	2 children	Active	Green	Yes	Yes	55%	Follow-up 9
2050	75	Male	Urban	Teacher	High School	\$40,000	Good	2 children	Active	Green	Yes	Yes	60%	Follow-up 10
2055	80	Male	Urban	Teacher	High School	\$42,000	Good	2 children	Active	Green	Yes	Yes	65%	Follow-up 11
2060	85	Male	Urban	Teacher	High School	\$45,000	Good	2 children	Active	Green	Yes	Yes	70%	Follow-up 12
2065	90	Male	Urban	Teacher	High School	\$48,000	Good	2 children	Active	Green	Yes	Yes	75%	Follow-up 13
2070	95	Male	Urban	Teacher	High School	\$50,000	Good	2 children	Active	Green	Yes	Yes	80%	Follow-up 14
2075	100	Male	Urban	Teacher	High School	\$52,000	Good	2 children	Active	Green	Yes	Yes	85%	Follow-up 15
2080	105	Male	Urban	Teacher	High School	\$55,000	Good	2 children	Active	Green	Yes	Yes	90%	Follow-up 16
2085	110	Male	Urban	Teacher	High School	\$58,000	Good	2 children	Active	Green	Yes	Yes	95%	Follow-up 17
2090	115	Male	Urban	Teacher	High School	\$60,000	Good	2 children	Active	Green	Yes	Yes	100%	Follow-up 18
2095	120	Male	Urban	Teacher	High School	\$62,000	Good	2 children	Active	Green	Yes	Yes	105%	Follow-up 19
2100	125	Male	Urban	Teacher	High School	\$65,000	Good	2 children	Active	Green	Yes	Yes	110%	Follow-up 20
2105	130	Male	Urban	Teacher	High School	\$68,000	Good	2 children	Active	Green	Yes	Yes	115%	Follow-up 21
2110	135	Male	Urban	Teacher	High School	\$70,000	Good	2 children	Active	Green	Yes	Yes	120%	Follow-up 22
2115	140	Male	Urban	Teacher	High School	\$72,000	Good	2 children	Active	Green	Yes	Yes	125%	Follow-up 23
2120	145	Male	Urban	Teacher	High School	\$75,000	Good	2 children	Active	Green	Yes	Yes	130%	Follow-up 24
2125	150	Male	Urban	Teacher	High School	\$78,000	Good	2 children	Active	Green	Yes	Yes	135%	Follow-up 25
2130	155	Male	Urban	Teacher	High School	\$80,000	Good	2 children	Active	Green	Yes	Yes	140%	Follow-up 26
2135	160	Male	Urban	Teacher	High School	\$82,000	Good	2 children	Active	Green	Yes	Yes	145%	Follow-up 27
2140	165	Male	Urban	Teacher	High School	\$85,000	Good	2 children	Active	Green	Yes	Yes	150%	Follow-up 28
2145	170	Male	Urban	Teacher	High School	\$88,000	Good	2 children	Active	Green	Yes	Yes	155%	Follow-up 29
2150	175	Male	Urban	Teacher	High School	\$90,000	Good	2 children	Active	Green	Yes	Yes	160%</	

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
 CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCCACCCGA
 CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
 CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC
 CTGCCACCTCAACGTCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC
 TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC
 TGAGGAGATGTTCTCCAGTTCGCGATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
 ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTG
 CAGCCGGAGGATGAGGGGATTACAACTGCTACATCATGAACCCCCCTGACCGCCACCGTGG
 CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
 CCGTGATTGTGGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTTCATCTTGGTGCTGATGGTG
 GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
 GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC
 CTGCAGCCTCCCGTGTCCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCTGCTGCTCG
 CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCG
 ACTTCGTATCTCCACCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
 TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG
 GGGAGGCAGGAGGCACATGTGAGGGTCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
 GGAGGGCCGCTGTACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
 GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG
 TGCTCCTCCCCTGCTCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
 AACTTGAGGGGCATGTATAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG
 CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGGCCTCGTTTCCATT
 GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
 ACTGGAAGAGCAGCTCCAGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC
 AGTTTCAAAGTCAGTCAAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTGTGCTGCAG
 GCTCTGCCTTCTCCATGGGGTAACCACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
 GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTT
 GCCCTTGGTGGGGTTTTCCACCTGGCTTTTGGCTACAGAGAGGGGAAGGGAAAGCCTGAGGCCG
 GCATAAGGGGAGGCCCTTGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG
 CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC
 ACAGTGGCTCACGCCCTGTAATCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT
 CTGTTTAGTAGAAATGGGCAAAACCCCATCTACTAAAAATACAAGAATTAGCTGGGCGTG
 GTGGCGTGTGCCTGTAATCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
 GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTACAGCCTGGGTGAC
 ATAGAGAGACTCCATCTCAAAAAAAA

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

protein sequence

[illegible]

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTTTAGCATCCAACCATCCTCCCTTGTA
 GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
 AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
 TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCACCCCTCAACGTCC
 TCAATGGCTCTGACGCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
 AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
 TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
 GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
 TTTACAACCTGCTACATCATGAACCCCCC

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCC

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA

FIGURE 58

TGCGGCGACCGTTCGTACACCATGGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT
 TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGACGTCACCCCCAGTGGTGTGCTGGTCC
 CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA
 CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAAGTGTGCTGCTGCTGCTCATCATTTGACTGCTGGATTGACAATA
 TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG
 GGAAGACCTTCTCACTGGAGTTCTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA
 GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG
 AAAACGGGCCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC
 TGGTTGCCCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCCTGGAAGGACAAGT
 ATATCCGGGCCTTCTGTGCTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAAGACCTGCGCGTCTGGCTTCAGGAG
 ACAACAACCGGATCCCAGTTCATCGGGCCCCGTAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCACAGCTGGC
 TGCTGCCCTACAACATACATGGTCACCTGAGAAGGTGTTCGTGCAGACACCCACAATCAACTACACACTGCGGG
 ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
 AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT
 ATGAGAGCTTCCCTGACCGTGACCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACTTGAAGAGTGCCC
 TGCAGTGCCAGGCCTGGCAGAGCCGCGAGGACCAAGTGTGTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG
 AGATGCTGGCCAACGCCACCACCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCCCGACTCCTGTGCCACAGGA
 CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTGATGGCCACGCGTTTTGCAAAGTTTGTGA
 CTCACATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGGAAGTGTGTTTTGTTATCCTTTCTCT
 GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGGA
 ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCCAGTCCCTGCCTGGGGCCATG
 TGTCCCCCTATTCTGTGGGGCTTTTCATACTTGCTTACTGGGCCCTGGCCCCGAGCCTTCTATGAGGGATGTT
 ACTGGGCTGTGGTCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTGGGTGACCCTTCCCACACACCA
 GCCACAGATAGGCCTGCCACTGGTCATGGGTAGCTAGAGCTGTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
 TGAAGTGGCTTCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGAGTTTGTGCGTTCTTCGTGGTTCCCAGGC
 CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG
 CCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC
 CTCCCTTACCCCTGGGACTGTGTTCCAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGA
 GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCACCATCA
 CACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCAGGGCTGAGGATGGGGCTCCTATCCAC
 CCTGGCCAGCACCCAGCTTAGTGTGGGACTAGCCAGAACTTGAATGGGACCTGAGAGAGCCAGGGGTCCCC
 TGAGGCCCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT
 CAGGGCTGCCCTTCATGGCAGTAGGCTTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT
 GGGGTTCCCAAAGACGCCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG
 TTGCATACATGCCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG
 GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQORSAVSTSWLLPYNYTWSPEKVQVQTPTINYTLRDYRKFFQDIGFEDGWL
MQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAGTGCCA
GCCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGA
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCCGGTCCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGTCTCATGGCACTTCCTCCTTG
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTG
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

Figure 60

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYGSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIGDLLFSALWTFLWFVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FIGURE 62

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
CCCGTGGCCGAGGCCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG
ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGTACCTCCGCCTGGTGCCCTGTTTGTGCTGCTG
GCCCTGCTCGTGTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGC
CAGGTGTACTCAGGCAGTCTGCGTGTAATCAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGTGCC
TTCCGCAGTGAAACCCGCCAAAGCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACCTTACTAC
AACTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTTATTCTCCAAATCCCCGAG
CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC
TCGGCTGCCGTCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA
GACATAGCTGCATTGAATTCACGCTGGGTGTTACCGCTACAGTACGTGGGCCAGGGCCAGGTCTCCGGCTG
AAGGGCCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCG
CTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTC
ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTGGGGGGCCATCATGGCGGT
GTCTGGAAGAAGGGCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT
GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCAGGGCGTCTCAGCACCCCGTACTTCCCCAGCTACTAC
TCGCCCCAAACCACTGCTCCTGGCACCTCACGGTGGCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC
TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT
GGCTTGCGCATCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC
TCCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTGTACAAACAGTCCGACCCCTGCCCTGGA
GAGTTCCTCTGTTCTGTGAATGGAATCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCAACCGCCTGGAT
GAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCCAAGGTCTGT
GATGGGCAGCCTGATGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCC
TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGCACTGTGATGGGCGGGCCGACTGCAGGGACGGC
TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCACTGTTGGTGGAGCTGTGTCTCCGAG
GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGTGACACATCTGTGGGGGGGCCCTCATCGCTGACCGC
TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGTGTGGACCGTGTTCCTGGGC
AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCAC
GAAGAGGACAGCCATGACTACGACGTGGCGCTGTGTCAGCTCGACACCCGGTGGTGGCTCGGCCCGCGTGGC
CCCGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG
CGCGAGGGCGGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCACTTGATCCACAGGACCTGTGCAGCGAG
GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGT
GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTG
GGCTGTGGCCGGCCTAACTACTTCCGGCTTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG
ACCTGAGGAAGTGGCCCCCTGCAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGCCAAGCAGG
GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC
CTGATGTCTGTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCTGAGGACC
CAGGCCACACCCAGCCCTTCTGCCTCCCAATTCTCTCTCCTCCGTCCCCCTTCTCCACTGCTGCCAATGCAAG
GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG
CTGTTTGGGCAGCCTTGCTTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCCTGGTCTAACTTGGGATCTGGGAAT
GGAAGGTGCTCCCATCGGAGGGGACCCCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAGCCAA
AAGGTGGGGAAGTCTGACTCCAGGGTCTTGCCCCACCCCTGCCCTGCCACCTGGGCCCTCACAGCCAGACCCCT
CACTGGGAGGTGAGCTCAGCTGCCCTTTGGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLKGPDLASSCLWHLQGPDLML
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLNRLDSQGVLSSTPYFSPSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDCGQPDCLNGSDEEQCQEGVPCGTFTTFQCEDRSCVKPNPQCDGRPDGRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAACHCFQEDSMASVT
WTVFLGKQVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCTGGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGA CT CAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAAGTGGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

[illegible][illegible]

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

protein: 56021001

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCTCCCCCGC
TTCCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGAGCAGGCCAGACCAGGGGCGCTCG
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGC GGCGGGACGAGAGAAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCGCGACCCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG
GCACCTCTGGACAGCCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCCTTACAGA
GGCCCCCTGGTCCGGGACAGCCGACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG
AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCTCCTGCCCTTGCAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCCACCCCCAGT
CCTGCCATTGGCTGGCCTGGACCCCATGATGGCCGGCGGCTGGCCGTTCACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCTTGGGACAGACCCCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT
CTGGTGCCACAGCCTGCTACCTGCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTTCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
CTTCCTACGGGCAGCTCATTTGCCAGGGTGCCATCCACCTGTAGAAGACTTTCTACAGAGAATCTAATGATA
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCCGTGCTCAGCGGGGCGGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGTGGGGCTTGCTCCCTCGAA
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCCTTGGGCCCCTAGATG
GTGGCACAGGTCAGCCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA
AGGCTCCCCCTCCCATCTGTAGCAGCTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCCTAGAGCCATCACTATTGCTGAGTGGTGACGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGAGCCCCCTGGACCCCAACAGCAGTCTTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACTTTTAGAGGTGGGTGAGCCTCCCTCC
ACCACTTCTTCCCTGTCCCTGGATTTTCAAGGACTTGGTGGGCCTCCCGTTGACCCCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACCTGCTCCCCACGCCACCACCATTTGGGTGGCTGTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAACCTAGAGA
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTGGCATCCACAATCCCTCCTACAGGGCCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTIQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEETFQCLNHRCSVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRP
VPSLPCNVLTLEDIFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRFTALDLGFGDAVH
VYDGPGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPCADGSDEWDCS
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGPGARRRQGRRLMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLP SLGPPGPTRSPPGPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACCTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAAGAAGTTTTGTAAATTTTATATTACTTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAA

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 70

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCGCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACCTTGTGACAGCAGTATGCTGTNTTGCCGAC

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FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCAACGCTGCTGCGCCTGCCCCAGAAGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTACG
CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTATCTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTCGTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFDLSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLR
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLPFRC
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCCTGTGGCCGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCTGAAGGCATGTGCCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCACTGTGCGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCCATCTTCTCTAAGCACCCCCCACCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAAA

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGA YVLVYYNLVKAPPCGGMGNLRGRTAVVTGANS GIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLD FKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELF LRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDRAAHLWEASKRL
AGLGPGEDAEPEDEDPQSEDSEAPSSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG
GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC
CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTGTGCTGAATGGGCAGCCCTGAGCATGGTGCCCCCAGAC
CCACACCACCTCCTGCCTGATGGGACCCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACAGATGGCCAG
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT
CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG
TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG
GCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGTTCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG
ACCTACATGTGTGGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCC
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTGAGCTGGAAAATGTGACACTGCTGAACCCGGAT
CCTGCAGAGGGCCCCAAGCCTAGACCGCGGCTGTGGCTCAGCTGGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA
TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC
GGCTGGCAGAGCGCAGAGCTTGGAGGCCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC
CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAGAGTGCCAGTGCCCCACCTCAGGAA
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAATGGCATC
ATCCGTGGCTACCAAGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAAGTGGACTGTAGTTGGTGAGCAG
ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAGTGGCTGCAGTCACTGGTGTGGAGCT
GGGGAGCCAGTAGACCTGTCTGCCCTCCTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCAGTGAGCAT
GGTCCCTGGACCCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTGATTGCCACCTGCGGTGTTGCACTC
TGGCTGTGCTTCTGGGCACCGCCCTGTGTATCCACCGCCGCGCGGAGCTAGGGTGCACCTGGGCCCAGGTCTG
TACAGATATACAGTGAGGATGCCATCCTAAAAACAGGATGGATCACAGTGACTCCCAGTGGTTGGCAGACACT
TGGCGTTCCACCTTGGCTCTCGGGACCTGAGCAGCAGCAGCCTCAGCAGTGGCTGGGGCGGATGCCCGG
GACCCACTAGACTGTCTGCTCGTCCCTTGGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCTGCTTCCAGACAC
AGCACTTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAGCT
GTCAGGCGCCTCCACCCAGCTGGCCAGCTCTCCAGCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGAGG
GGACTCTCTTCTCCCGCTTGTCTCTGGCCCTGTCAGAGGCTTGAAGGCCAAAAAGAAGCAGGAGCTGCAGCAT
GCCAACAGTTCCTCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCC
AAGAACCCTTTCCCAAAGCCAGGAGCTGTGCCCAAGCTCTGGTTGCTGGCGGGCCCTGGGACCGAAACTCCTC
AGCTCCTCAAATGAGCTGGTTACTCGTCACTCTCCCTCCAGCACCCCTCTTTCTCATGAAACTCCCCAACTCAG
AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC
CTTAGCCCCCTGCAGTCCCCCTAGCCCCAGGCTCCTCCCTCTCTGGCCCCAGCCAGCTTCCAGTGCCTGTCC
AGCTCCTCACTGTCACTCCCTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA
CTCAGTGAGGTGAGGAGACTCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCCAAGGGG
GGAGTCTTGCTGTGCCACCTCGGCCCTGCCCTACCCCCACCCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGCTCCTCCGATGGCTCCTTCTCTCGCTGAT
GCTCACTTTGCCCGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCAGGGAGGCAGACTGC
GTCTTCATAGATGCCCTCATCACTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCCTG
TGGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCCAGCGGCTGGGAAGGGGGATGCCCTCCC
TGGCCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCTGATGCCCAAGGCTGGTGTCTCTCCT
GTAGATTACTCTGAACCGTGTCCCTGAGACTTCCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG
ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG
TTCTCCCTCCACGATTGTGAAAAACAAATGAAAAACAAATAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA
ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCTCTGTGCCATCCACTCCCACCACAGGTTGTTTGGC
CTGAGGAGCAGCCTGCCTGCTGCTCTCCCCACCATTTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCCTTT
GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGAGGCCCTCTCAGCCTTACCT
GGGCCCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG
AGGCACTGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG
TATGAGACCGTAGGTCAAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGP GPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLLP
DGTLLLLQPPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPG RHTVSGGSLLMARA EKSDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLE NVTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVA AVTGAGAGEPSRPVCLLLEQAMERATQEPSEHG PW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLL PDTST
FYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRLSSPRLSLAPAEA
WKAKKKQELQHANS SPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFP HETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCP RPRCLTPTPSEGLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSH TQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCACGGTGTCCAGCGCCCAGAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT
CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA
ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
TCTTTACTGATCTCTCTGTTCTTTCAGGACCCTGCTGTCTCCTCCCTCCCCTTCTCCCAC
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAGCTCAGCAAACCCAGCCCC
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGC
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGCTGCTGAGCCTTCTGTCAGC
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC
CCTTCCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCTCCTCCTCCTTGCATGTTCCA
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCTCA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
CTCATGCCCAGTGTGCGACCCCTGCCTTCTCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
GACTCTGAATTCTAACAATGCCAGTGAAGTGTGCGACTTGAGTTTGAAGGCCAGTGGGCCTG
ATGAACGCTCACACCCCTTCACTTAGAGTCTGCATTTGGGCTGTGAGTCTCCACCTGCCC
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGAAGTCCCTGAGGCCTGCTAAG
TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTACTTGCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTTCGGGGGTGGTGGTAAAGTA
GCACAACTACTATTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
GCTGCCCAGGCTGGAGTGCAGTGGCAGATCTGCAAACCTCCGCTCCTGGGTTCAAGTGATT
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGAC
CTCAAATGAGCCTCCTGCTTCACTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
TCTGGCCCTATTTCTTTTAAAAAGTGAATTAAGAGTTGTTTCACTATGCAAACTTGGAAAG
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
TATTTCTGTTTTGTGTTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
TTTACAGAGCAATTATCTTGTATATACTTTGTATCTGCTTTTCCACCTTATCGTTCC
ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA
GCTGCATAAAAAAAAAAAAAA

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPPEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSTRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFV
FPGPCCPPSPSPSTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCAACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTNPVNPVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCDP

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCTGCGTTC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCTGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG
GAAGGCCATCCTGACACACATGCGGGTGGGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTTTTGTTCTGGTTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTCATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTTATTTAGCCCTTACATGGACAGCTAGA
GGTTGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCCTGGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCCGAGTCACCTTTCACAGCGCTGTTTCTCCATGAAACTGAAAAACACACAC
AC
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTC

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPLVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQS FVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG
GTGCCCTGAAGGAGGAGGTTCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAAGTGCCTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTCAAGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACCTGCTTGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAEELGEAQAKLMEQESALR
ELRERVLTQGLAEAGRGREDEVTELFRALAEAVRLQNNSCEPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCACGTCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCCGGCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCGGCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCGCGTCCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCTCTCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTTCGTCTTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGCAGCCCCTGGGGCCCCCG
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG
TCCAGGGGCCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFGVDSLDCDGRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPAN SFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA
NNGSPCPELEEEAECVPDNCV

Important features:

Signal peptide:

amino acids 1-26

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FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTTAGTGTTTGGTGTCCCTGTCTTGCGTGA
TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAATA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGAGAAATTTT
ATCCAACCTTTGTTTGGGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTTCATTCACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTTCGAGCAGATGAAC
TAACAATAAGCATAACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAAATAAAAAGCTGT
GAGGTTTTGTTTAAATCCTTTTGATGACATCATTCGAAGGAAATTAAAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACCTTTAGCAG
CAAAACAAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAGAAGATAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTTTTGCAAATGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTT
TCCACAAAAA

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNRSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKS
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSTREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQDSDTFEIYDPRNPVNKRRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCTGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTTCGCCTTGCTGACGGCGTCG
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
CTCCTTCAAGTGGTTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAA
GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTCGCCAGGCTGGAG
TGCAGTGGCAGCATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG
ATGTACGTCAACACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC
GAGAAAGTGGTGCTGGTGTTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGGCCAGTCCGCG
GGGGCCATGAGCATCTCAGGACTGATGATGTCAACCCCTAGCCTCGGGTCTCTTCCATCGGGC
CATTTCCAGAGTGGCACCGCGTTATTCAAGCTTTTCATCACTAGTAACCCACTGAAAGTGG
CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCTTATAATATCACCAAGGAGCAGGT
ACCCTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTTTCGTGTATGCCACACTGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TATGCAGGAAGGAGCCAAAGAGGGGTTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC
TGACATCCCATGATGCCCCCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT
CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC
CCCTGTCACTGCACCCAGCTTGGCATTATACCATCCATCCTGCTCAACCTTGTTCCTGTCTGT
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPPFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSCLYLNQVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDD
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.2	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.7	0.3	0	1
Sleep quality	0.6	0.4	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.6	0.4	0	1
Depression score	10.5	5.0	0	30
Anxiety score	12.0	6.0	0	30
Quality of life score	75.0	10.0	50	100

[illegible]

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLEFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCTCTCTCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTCTATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACCTTTTCTGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTTCGCAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA
AAAGAAAGTGGATTTTGTAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCTTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTTATTAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCTTCCATATTATGTATTTGAAGTTTGTGA
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCAATTTGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA
TTTGGGTTTATTTTTTTTACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTGA
GAAAAGTGAAGATTTTCAGAGAGAATATATTTCCAATATGATGATGAAGGGGTGGAGAAGAAG
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCCTCTTTTGGATTCCCTCCAGACCTACGCTTTTGGAGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAAATTTTTTAAAAGTGCTAATGTGTATTGCAACCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCTATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATG
TAGGAAGATATTTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT
TTAAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLOQQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSLSD
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEHHHFYFNLSVEDTMNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPD SAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESASVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA
 AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
 CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
 TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
 NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
 AGCATTGAAGAGGATGATTTCGCAAACATTTGACATTATT

[illegible]

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGGCGGCGCAGCGAGCAGGGCTCCCCGCCCTTAACCTTCTCCGCGGGG
CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCCTTCTGCGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACATTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCTATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCAGT
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCC
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGAACACAGAGGCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAAACATTAGGAC
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCA
ATATAGGAGGGAAGATTTTTCATTTGTATTACTGCTTCCCATTTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTCTATTAAAA
ATAGACAGTAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAT
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC
TTATATACATATGTAACAGTCAAATATCATTACTCTTCTTCACTAGCTTTGGGTGCCCTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCACTCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG
ACCAAAGTGATAAATTCCTGTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAACT
ACCTTTTTGTTCCTTCCCTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTTA
TATCTTCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT
CACTGCCTTCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACTTCAT
GTGGTTCAGTGCCCTTCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC
CTTCATGTGGCTCAGTGCCCTTCTCTCTCTACCAGTCTATTTCCATTCTTTTCTGCTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTTGGTTTTGTAAATTTAAAAAGTGCTAT
ACTAAGGGAAAGAATTGAGGAATTAACCTGCATACGTTTTGGTGTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI¹LAFLGWIGAI²VSTALPQWRIYSYAGDNIVTAQAMYEGLWMS³CVSQSTGQI⁴
QCKVFDSL⁵LLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLE⁶DEVQKMRMAVIGGA⁷
IFLLAGLAILVATAWYGNRIVQEFYDPMT⁸PNARYEFGQALFTGWAAASLCLLGALLCCSC⁹
PRKTT¹⁰SYPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT
GTTCCCTGTCCC

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FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

Figure 100

FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTGCGA

FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCCCTGTCCC

FIGURE 103

Parameter	Estimate	Standard Error	t-Statistic	p-Value
Intercept	1.0000	0.0000	1.0000	0.0000
Age	0.0000	0.0000	0.0000	0.0000
Age squared	0.0000	0.0000	0.0000	0.0000
Age cubed	0.0000	0.0000	0.0000	0.0000
Age quartic	0.0000	0.0000	0.0000	0.0000
Age quintic	0.0000	0.0000	0.0000	0.0000
Age sextic	0.0000	0.0000	0.0000	0.0000
Age septic	0.0000	0.0000	0.0000	0.0000
Age octic	0.0000	0.0000	0.0000	0.0000
Age nonic	0.0000	0.0000	0.0000	0.0000
Age decic	0.0000	0.0000	0.0000	0.0000
Age undecic	0.0000	0.0000	0.0000	0.0000
Age duodecic	0.0000	0.0000	0.0000	0.0000
Age tredecic	0.0000	0.0000	0.0000	0.0000
Age quattuordecic	0.0000	0.0000	0.0000	0.0000
Age quindecic	0.0000	0.0000	0.0000	0.0000
Age sexdecic	0.0000	0.0000	0.0000	0.0000
Age septendecic	0.0000	0.0000	0.0000	0.0000
Age octodecic	0.0000	0.0000	0.0000	0.0000
Age novemdecic	0.0000	0.0000	0.0000	0.0000
Age vigintic	0.0000	0.0000	0.0000	0.0000
Age unguic	0.0000	0.0000	0.0000	0.0000
Age duodevigintic	0.0000	0.0000	0.0000	0.0000
Age tredecimvigintic	0.0000	0.0000	0.0000	0.0000
Age quattuordecimvigintic	0.0000	0.0000	0.0000	0.0000
Age quindecimvigintic	0.0000	0.0000	0.0000	0.0000
Age sexdecimvigintic	0.0000	0.0000	0.0000	0.0000
Age septendecimvigintic	0.0000	0.0000	0.0000	0.0000
Age octodecimvigintic	0.0000	0.0000	0.0000	0.0000
Age novemdecimvigintic	0.0000	0.0000	0.0000	0.0000
Age vigintivigintic	0.0000	0.0000	0.0000	0.0000
Age unguicvigintic	0.0000	0.0000	0.0000	0.0000
Age duodevigintivigintic	0.0000	0.0000	0.0000	0.0000
Age tredecimvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age quattuordecimvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age quindecimvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age sexdecimvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age septendecimvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age octodecimvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age novemdecimvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age vigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age unguicvigintivigintic	0.0000	0.0000	0.0000	0.0000
Age duodevigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age tredecimvigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age quattuordecimvigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age quindecimvigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age sexdecimvigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age septendecimvigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age octodecimvigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age novemdecimvigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age vigintivigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age unguicvigintivigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age duodevigintivigintivigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age tredecimvigintivigintivigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age quattuordecimvigintivigintivigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age quindecimvigintivigintivigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age sexdecimvigintivigintivigintivigintivigintic	0.0000	0.0000	0.0000	0.0000
Age septendecimvigintivigintivigintivigintivigintic	0.0000	0.0000	0.0000	

[illegible][illegible]

FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTG CAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCCCTG

[illegible]

FIGURE 106

TTCCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCCAAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

[illegible]

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNATGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTCTGCGAA

FIGURE 108

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC
CGCGTAGACCGACCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCGGTGCCCCG
ACCGGTCCCCGCTTTTGTAAAACTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGT
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCCTGAGCCTCGAGCCGCAGCACGAGCTCAAATTCCGAGGTCCCTTCACCGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGGTTTCAGTCTATGTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAAACCGGAAGACCTTATGGATTCAAAACCTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
GATAAACACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAAACAAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGC
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTCTTTA
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
TCTTAAATGACACCCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT
GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTG
CTTTCGCTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTAAGTGCATAAGTGAGAGGCGTGTGT
TGACTGATTGACCCAGCGCTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGAGTGAAGTCAAACCTGTTATTAGAGATGTTTAAATGCATA
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTTCCAGCGCCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGAAGTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHCLKFRGPFTDVVTTNLKLGNPDRNVCFKVKTAPRRYCVRPNSGIID
AGASINVSVMQLQPFYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCC
CCAAAATTAAGAATTCTTTTGTCATTTTGTCACATTTGCTCTATGGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAAATGAGC

Figure 110

FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCN TTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTA CTGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAC TGTATTTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

Figure 111

FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

[illegible]

FIGURE 113

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTTANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTG
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

Figure 113

FIGURE 114

TGCTTTC CGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTCA
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAC TGTTATTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTT CATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

[illegible]

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC
GGCCCAGGCTGCTTTCCGTGCTTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

Figure 115

FIGURE 116

[illegible]

FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCA
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAATAATATGCTGCTTTGGTTGATATTTTTCACC
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACCTTGAGAAA
GGTACCCCGGATTGTGAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC
CTTTCTGAATTGGAGGATTATCTTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCAAGCATCTTGACAAA
AGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAAATCTGGCCGGGGT
AGAGGATTGCCGAAGGGAGGCCCTTCTTTTCAAGTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA
TGCCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTTCGGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC
GCAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTTCAAGAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCTTAAATAACGCCCAGATTTGCCTCTGGATTACCGG
GAACGATGCCAATTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT
GAACTCTGTCAATAGCATTTCACATTTTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTTAGTTTAGTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA
CAAACCTAATAACTGTTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAATAAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSRRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAACVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDSNLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCAACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT
ATATCTGGAACCAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGGTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGGAGGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPCSLKCQ
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDLHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

protein sequence

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAAC TCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGGTTCTGTTGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA
GGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAACTGGCTAACATTCTTTT
TACCAGGGAAGTACCGCCGCGCTTAGAAGGCACAAATGTACCGTCAATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGTGATGGGCTTTTTTTCAAACTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAAGTTGTTACTTGAAGAAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTACTGAAAAATTATTTT
TGGGATAAGAGAATTTTCAAGCAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAATAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGAATAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEAAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNH LGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEG TNVTNVNLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	1500	500	1000	2500
Health status	0.5	0.5	0	1
Smoking status	0.5	0.5	0	1
Alcohol consumption	0.5	0.5	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.5	0.5	0	1
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Depression score	10	5	0	30
Anxiety score	10	5	0	30
Quality of life score	50	10	30	70

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTACGGAC
CCCAGCGTTACCATGTCATCCTGCCGTCCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA
ATATCATTTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCTTGGAAGCACTCAAGCAATTCG
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAACTTG
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATTCTATGTGTATTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFPTVTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQOKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREI
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

protein: 5306700

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

Figure 126

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTTCGCCGCNGGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCCAGCCCTTTCTTAACCC
AACCCAACCTAGCCCNGTCCAGCCGCCAGCGCTGTCCCTGTCNCGGANCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTTACTCCTGTAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTCGTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCTCAAATTGTTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

Figure 1 consists of 12 bar charts, labeled (a) through (l), each representing a different variable. Each chart compares the percentage of respondents in 1995 (white bars) and 2000 (black bars) across various categories. The variables are: (a) Age, (b) Sex, (c) Education, (d) Income, (e) Employment, (f) Religion, (g) Political affiliation, (h) Party affiliation, (i) Attitude towards the environment, (j) Attitude towards the economy, (k) Attitude towards the government, and (l) Attitude towards the military. The charts show shifts in the distribution of responses for each variable over the five-year period.

FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTA TACTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG
TTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTTCTTTAGT
GCAATACAATAAAACTCTGAAATTAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG
AATCCCCTTGTA TACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTTATCTTCTAGCATTTTT
T TACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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FIGURE 131

CGGACGCGTGGGGGAAACCCCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAAGTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCCACTCCTCATAGAGCTTTTAAAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSILWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESECTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

Sequence: 580600

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC
TGAAGTGAACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

Figure 133

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCG
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

530,000

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGGCCGCGGCTG
GGGATTCTTGTTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAATAATGGAATGTCATCTACGAAGAAAAGTGTTTTAAGCCAC
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGAAGTAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTTTTGCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC
TCAGGAACTTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGAATTTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTCCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

sequence

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGTATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAATAATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGTTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTACAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW

DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

protein sequence

1110 1100 1090 1080 1070 1060 1050 1040 1030 1020 1010 1000 990 980 970 960 950 940 930 920 910 900 890 880 870 860 850 840 830 820 810 800 790 780 770 760 750 740 730 720 710 700 690 680 670 660 650 640 630 620 610 600 590 580 570 560 550 540 530 520 510 500 490 480 470 460 450 440 430 420 410 400 390 380 370 360 350 340 330 320 310 300 290 280 270 260 250 240 230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10 0

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCC
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGGCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACTGGGAAATTCATCTCATCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATAACAACCTTCGTGTACAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTCTGTCTGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
TGGTCTCTCCAGACACCTTGAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT
CTCATAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGA CTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGAGAGAGCCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAAAAAAA

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHELLMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS AW
SILKHPFNRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREP GAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLV LALFAFVGFM LILV
VVPLFVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT

FIGURE 144

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGTGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGGGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG
AGGTGCAGCTCATTCACCTTCAACCAGGAACTCTACGGGAATTTACAGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCACTACCGCCTGCATGTGGA
TGGTGTCCCCCATGGTTCGCTGAGACTCCCCTTCGAGGATTGCACCCGCCCGTCCTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAACAAAGCTATTAAAGGGACAGAATACTTA

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLRDITITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSSTPPCSE
TVTWILIDRALNITSLQMHSRLRLSQNPSSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPR
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 145

FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTC
 GTTCGTGTCCCCCGCCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
 GCAGCTCCCTTCCACCCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCCTGCCATTTCTTCCAGGTTGAGGGAGC
 CGCAGAGGCGGAGGCTCGCGTATTCTTGCAGTCAACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
 GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT
 CACCTCTCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
 ATCCTGAGGTCATTTCATTATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGCTGTTTATGGCTAGA
 GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGATAGCCAAACACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
 AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
 TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA
 CAGGTCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCTAATCATGAACATCTGGGGGAG
 ATATGGCCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA
 CATGGGCGGCCCTGTTCTGCTTGGCCACCTAGTTTTTGGAGGGGGCTGTAGAGAAAATCTGTGTACAAAGAAGGG
 TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCT
 TGTGAAGTAAGATTAAAGAGATCAGTGCAGGAACAACTGCAATAGGTACGAATGTCTGTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTATCAAGTCCAATAGA
 AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTACAGTCTCTAAAGTAACAGTTTCAAGCTGTG
 ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTATAAGCCTGCTTACATTGCCCCAAGAGTATACTGTCTCT
 CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATTGGAACCTCGAGTTTATTCTGATCTGTCCAGTATC
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
 AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT
 AGAGTGTGTTGCTGTTGTGTTGAAACTGAATACCTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCACTATTTTTCAGCCCCAAAAGGTGCCAAATGCATA
 TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTTGGGAAAAGTAATGAAAATATAATGG
 TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
 GTTCTACGTTTTCATATATTATATGGTGTCTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
 GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACTGAAAGAAACCTTATCACATTTTCCCC
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTCT
 TGTTAATTTAGGCATATAGAATATTAAATTTCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC
 CAAATGAATCTGTAAATGTTTGGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
 ATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
 AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
 GAACAAAGATGAACATAATGTATTACATTACCATTTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATAA
 ATATTGCCATATCATGGTACCTATAATGGTGTATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA
 AATCTGTAAATGTTAGTTTTTGGTAATTTTTTTTCTGCTGGTGGATTACATATTAAATTTTTTCTGCTGGTGGAA
 TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAAA

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVT'TVLFMARAIPAMVVPNATLLEKLLLEKYMDEDEGEWWIAKQRGKRAITDNDM
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLC
HNMNIWGQIWPKAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRY
YPPREEETNEIERQQSQVHDTHVRTRSDSSRNEVISAQQMSQIVSCEVRLRDQCKGTT CNR
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSES LQNPPGGKAFRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

CGGGAGACAAGCGCAGAGCGCAGCGCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCCGCCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCACGCCG
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCAACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATTAGGGTGAAAAACCTCAGAAGGGGAAAACCTCCAAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTTGCAGATTAAAGCCTTTC
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCCTTTTTAA
AAAATGCTTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGAGCAAAAACCTTAGGAGAAAAC
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT
GACCATGCGCCCTTTCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTGAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAAAA

FIGURE 149

MSLLPRRAPPVSMRLAALLLLALLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMWIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNANNEKRRVYEE

Signal sequence:

amino acids 1-34

FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCCGGTCTGCGTCATGTTAAACTCCAATGTCTCTCTGTG
GTTAACTGCTCTTGCCATCAAGTTACCCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG
CAAAATCCGGGGCCTAAGAACCCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA
TGCCTCACCCCCCACTGGAGAGAGGCGGTTTTCAGCCCCCAGAACCCCCGTCCTCTGGACTGGCATCCGAAATAC
TACTCAGTTTGCTGCTGTGTGCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT
TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTTAAACATCTACGT
GCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA
TATTCATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACT
AGGGTTTTTAAAGTACCGGTGACCAGGCAGCAAAAGGCACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG
GATTGAGGAGAAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC
CTGTGTGACGCTGTTGACCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTAGAGCGGCACCGC
CCTGTCCAGCTGGGCAGTGAACTACCAAGCCGCAAGTACACTCGGATATTGGCAGACAAGGTGCGGTGCAACAT
GCTGGACACCACGCACTGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC
GGCCACCTACCACATAGCCTTCGGGCGCGGTGATCGACGGCGACGTCATCCAGACGACCCCGATCCTGATGGA
CAAGGCGAGTTCCCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCTGAAGTTCGTGGACGGCAT
CGTGGATAACGAGGACGCTGTGACGCCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG
CTACCCTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTCATGTACACAGACTGGGCGGATAAGGAAAAACC
GGAGACGCGGCGGAAAACCTGTTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCGTGGCGCGCGACCTG
GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCTTCTATCATCACTGCCAAAGCGAAATGAAGCCGAGCTG
GGCAGATTCCGGCCCATGGTGATGAGGTCCCCTATGTCTTCCGTCATCCCCATGATCGGTCCCACCGAGCTCTTACG
TTGTAACCTTTTCAAGAACGACGTCATGCTCAGCGCCGTGGTCATGACCTACTGGACGAACCTTCGCCAAAACCTGG
TGATCCAAATCAACCAGTTCCCTCAGGATACCAAGTTCATTACACAAAACCCAAACCGCTTTGAAGAAGTGGCCTG
GTCCAAGTATAATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC
AACGAAAGTGGCTTTCTGTTTGAACCTCGTTCCCTCATTTGCACAACTTGAACGAGATATTCCAGTATGTTTCAAC
AACCACAAAGGTTCCCTCCACCAGACATGACATCATTTCCCTATGGCACCCGCGATCTCCCGCCAAGATATGGCC
AACCACCAAACGCCCAGCAATCACTCCTGCCAACAAATCCCAAACACTCTAAGGACCCTCAAAAACAGGGCCCTGA
GGACACAACCTGTCTCATTTGAAACCAAACGAGATTTATCCACCGAATTAAGTGTACCATTGCGGTGCGGGCGTGC
GCTCCTCTTCTCAACATCTTAGCTTTTGGCGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACTCACAG
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGTCAATCCAGAACGAAGAGATCATGTCTCTGCAGAT
GAAGCAGCTGGAACACGATCACGAGTGTGAGTGTGCTGCAGGCACACGACACTGAGGCTCACCTGCCCGCCAGA
CTACACCCTCAGCTGCGCCGTCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAAACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
CGGACATTTCCACCACTAGAGTATAGCTTTTGCCCTATTTCCCTTCCCTATCCCTCTGCCCTACCCGCTCAGCAACAT
AGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTGTCCCCT
GACTTAAGACAAAATGCAAAAAGGCAGTCACTCCATCCCGGCAGACCTTATCGTTGGTGTTCCTCAGTATTAC
AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTAAAAATAACTGCTTTAAGATCTCTACCA
CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAGGCCCCGGGTGTTTCCAACGTATGGAAGCAGCT
GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTTTAAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC
CACACAATGGATGGCTCTCTTAAGTGAAGAAAGAGTCAATGAGATTTTGGCCAGCACATGGAGCTGTAATCCAG
AGAGAAGGAAACGTAGAAATTTATTATTAAGAAGTGGACTGTGCAGCGAAATCTGTACGGTCTGTGCAAGAG
GTGTTTTGCCAGCCTGAACATATATTTAAGAGACTTTGT

FIGURE 151

MLNSNVLLWLTALAIKFTLIDSQAQYPVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPIWFTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGFEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVYPYV
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPVQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTE LSVTI AVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLT CPPDYTLTLRRSPDDIPLMTPNTITMI PNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCTGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCTCTACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTGGTGATTCTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCCTTGAAGTTGTTTGAAGTGCAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGTGTCTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACTTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCCTG
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC
AGAATTTCATAGCCCAGGCTGCCGTGTTGTTTGAAGTCAAGAGGCCCTTCTACTTCAGTTTTG
AATCCACAAAGAATTAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTCTGTTGGGTT
TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAAACT
TCTTCCCTGCCTTACCTTCTTTCACTCCATTCAATTGTCCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCTGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT
TACGATTTTTGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT
CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

[illegible]

><subunit 1 of .1, 348 aa, 1 stop

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ

LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSY

YYFGTSSITGDLSDNHDVISLKLFE~~LT~~VERTPEEEKLHRDVFLPSVDNMKLPEMTAPLPPLS

GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKR FY

amino acids 1-38

amino acids 310-329

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
CTGATGGTGGGTCTGTTAACTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
TGGGGTCTGGGCTCAGAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTCTTCCACCTGATCCCGGTGT
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCGACCTGTGACGGAGCCCCCTGTGA
CAGACCCCGTTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCCC
CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTATTTCGCCACGGAGACAGGTACCCACTGTATGTTCATTCCCA
AAACAAAGCGACCCAGAAATTTAGCTGACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAATGGAAGCTTTCA
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTTCGAAAGCCCTTGAACCTCTGCTCTTTACCCAAATCACC
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA
TCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA
GCCGGACCCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGTACTGGAAGAAGATTTATTTCA
GGCACCAGCCAAGTGGCTGTCTGCTCTGGAAGCTGCTATTGCCCGGTAAAGAAACAGTATCTGGAAAAGGAGC
AGCGTCGTCAGTACCTTACGTTTGAAGAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGCT
TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
GGGAAAGACGGGAGAAGAAATTTGACTTCGGGTATTCTCTCTGGGTGCCACCCCATCTGAACCAAAACCATCG
GCCGGATGCAGCGTGCCACCCAGGGCAGGAAAGAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT
CACCAGTTCTCAGTGCCTTGGGCCCTTTCAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGATTCTTTACAATGGCGTCGATGTCACTTCCACACCT
CTTTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAA
GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAAATTATTATGATGCATGTACAGGGAAGGATTCTAAAAGG
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC
TAAGGGTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTGTGGGAACCAAGATGGTTGGGGTTGAACAGT
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCAAGAGGAATAGAAGGTACTT
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCCAGCACACCTCAACCAAAATTTTTTTAATCTTAGACATT
TTTACCTTGTCTTGTGTTAAGAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGTAAAGG
GCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTATAACTACTCAACTCTGT
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA
GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCTCCAGTAACCTTCTGCTAGAAACA
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTTATAGTTTtaggAAAATATT
TTCTAAGACCAGTTTtagATGACTCTTATTCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
GAGGCTAGAAGATGAATTCAGGCACTTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA
ACTGGATTCATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTTAAATGCGTTTTTGGG
AGAACCTTGTCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
TGATTTCTGAACATAATGGTGCTAATTACAGAGAAATGGAAGTGAAAGTGAGATTCTCTGTTGTCTCGGCATTCC
AATTTTTCTCTTTGTTTTGTCCAGTGTTGCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAAGATAA

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFI RHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

protein = 330 a.a.

FIGURE 156

AAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCTTTTGAAGAACAGTACTGTGGA
GCTATTTAAGAGATAAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
GCCGCTGTTTACCAATCGGGGAGAGAAAAAGCGGAGATCCTGCTCGCCTTGACAGCGCCTGAAGCACAAAGCAGAT
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACCGGAGGAGCTCTGACTTCCCACTGTCCCATTCTAT
GGGCGAAGGAAGTCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAAATAATTCTGGAGGAAGATAAGAATGAT
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGCTGCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG
ATGCACCCAGATACGCTATTCACTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCGAGCTTTTCGCCCT
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
TCAATTAATCTAGACATTCTGATGGAGGATAAAGTGAAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
CGACAATGCGCCTTACTTTCTGTAAGTGAATTAGAAATAAAAATTAGTGAAGTGCAGCCACTGAGATGCGGTT
CCCTCTACCCACGCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG
CGAAGAAAAGGCTGCTCACCACCTGGTCCCTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGACACGCGTTTGCTCAGCCCGAGTACCGCGGAGCGTTCC
GGAGAATCTGGCCTTGGGACGCGAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT
GAGGTATTCCTTCCGGTATGTGGACGACAAGGCGGCCAAGTTTCAAAGTAGATTGTAATTGAGGACAATATC
AACAATAGGGGAGTTGGACCACGAGGAGTCAAGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA
TTCTGCGCGAGCCAAAGTCCCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCCCTCACCTCTCT
CGCCAGCTCGGTTCCCGAAAACTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAATGACCAAGATTCTGA
GGAAAACGGACAGGTGATCTGTTTCACTCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA
TAGTTTAGTACAGACATAGTCTTGGATAGGGAAACAGGTTCTTAGCTACAACATCACAGTGACCGCCACTGACCG
GGGAACCCCGCCCTATCCACGGAAGTCTATCTCGCTGAACGTGGCAGACACCAACGACAACCCCGCCGGTCTT
CCCTCAGGCCTCCTATTCCGCTTATATCCAGAGAACAATCCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA
CGACCCGACTGTGAAGAGAACGCCCAGATCACTTATTCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC
GTCTTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA
CTTGCAAGTGAAAGTGATGGCGCGGGACAAACGGGACCCCGCCCTCAGCAGCAACGTGTGCTTGGAGCTGTTCTG
GCTGGACAGAACGACAATGCGCCCGAGATCCTGTACCCCGCCCTCCCGACGGACGGTTCCACTGGCGTGGAGCT
GGCTCCCCGCTCCGCGAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC
CTGGCTGTCTACCGTCTGCTCAAGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
CACGGCGGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC
CCCTCTCTCCGCCACTGTACGCTCACCCTGGCCGTGGCCGACAGCATCCCCAAGTCCCTGGCGGACCTCGGCAG
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCCGGTCTCCTG
CGTCTTCTGGCCTTCGTCATCTTGCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCTGCTGCAGGC
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCTCGCACTTTGTGGGCGTGGACGGGGTGCAGGCTTTCTGCAGAC
CTATTCCCAGAGTTTCCCTCACCACGGACTCGCGGAAGAGTCACCTGATCTTCCCCAGCCCAACTATGCAGA
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAGCGAGCCCTTTTGTGTGAGGTGATTGCGTATTTTCTAAAGA
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTTTTTTTTAATTGCTCTGTCTCCCAAGC
TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTCCTAGGCTCAAGCAATTATCCCACTTTGCCT
CCGGTGTAAACAGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT
CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGGAGACAGCCTGACCAACATGGAGAAACCCGCTCTATACTAA
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAAT
TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTCCATTGCACTCCAGCCTGGGCAACAAGAGTG
AACTCTATCTCA

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAF AQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHD PDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAAVSCVFLAFVILL LALRLRRWHKSRL LQASGGGLTGAPASHFVGVD
GVQAF LQTY SHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNC SVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRD YRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGSLTPVIPVLWEAEAGGSPEVGSLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCAATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTTAGGTGGCAACTGGGTCTTT
ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTTCACTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT
CTGGTTC

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENF PDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGSDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCG
CGCGCCGCCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCCGCGCCCCG
GCCCCGCGCCCAAGTGAGCGCTCCGCCCCCGCGGAGGCCCGCCCCGGCCCCGCCCCCGCCCCG
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCTCGCGCGTCAAACCACTGATCCCATAAAAC
ATTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCCCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCCAGCCAGAGCCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCCGGGCCGTAGCGGCGGCGCCTGGA
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTTCAGTCCCCGACGCGC
CCCCCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCGCCCTACACACGCTGCACCTGGACCGC
TGCGGCCCTGCAGGAGCTGGGCCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCCGAGCGCGCCTTCCGTGGGCTG
CACAGCCTCGACCCTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCGATGCCTT
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCACGCCCACTCTGGGCCTGGCTGCAGAAGTTCCGCGGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCCGGTG
ACAGCCCCGCCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCGAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGCTGGACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG
GTCCTCCCTGATGGACGCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA
AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHG NRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCLQELGPG LFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHPHA FRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

Variable	Mean	SD	Min	Max	Skewness	Kurtosis	Normality
Age	38.5	12.5	25	65	0.1	3.2	0.95
Gender	0.5	0.5	0	1	0.0	3.0	0.98
Education	12.5	2.5	9	16	0.2	3.5	0.92
Income	1500	500	500	3000	0.3	3.8	0.90
Marital Status	0.7	0.5	0	1	0.1	3.1	0.96
Occupation	1.5	1.5	1	5	0.4	4.0	0.88
Health Status	0.8	0.4	0	1	0.2	3.3	0.94
Stress Level	2.5	1.5	1	5	0.5	4.2	0.85
Life Satisfaction	3.5	1.0	1	5	0.3	3.6	0.91
Resilience	4.0	1.2	2	6	0.2	3.4	0.93
Optimism	3.8	1.1	2	6	0.3	3.7	0.90
Emotional Stability	4.2	1.0	3	6	0.2	3.3	0.94
Self-Esteem	4.5	1.1	3	6	0.3	3.6	0.91
Life Purpose	4.0	1.2	2	6	0.2	3.4	0.93
Gratitude	4.2	1.0	3	6	0.2	3.3	0.94
Forgiveness	4.0	1.1	2	6	0.3	3.5	0.90
Empathy	4.5	1.0	3	6	0.2	3.3	0.94
Compassion	4.2	1.1	3	6	0.3	3.6	0.91
Kindness	4.0	1.2	2	6	0.2	3.4	0.93
Patience	4.5	1.0	3	6	0.2	3.3	0.94
Humility	4.2	1.1	3	6	0.3	3.5	0.90
Generosity	4.0	1.2	2	6	0.2	3.4	0.93
Modesty	4.5	1.0	3	6	0.2	3.3	0.94
Politeness	4.2	1.1	3	6	0.3	3.6	0.91
Respectfulness	4.0	1.2	2	6	0.2	3.4	0.93
Responsibility	4.5	1.0	3	6	0.2	3.3	0.94
Reliability	4.2	1.1	3	6	0.3	3.5	0.90
Integrity	4.0	1.2	2	6	0.2	3.4	0.93
Honesty	4.5	1.0	3	6	0.2	3.3	0.94
Trustworthiness	4.2	1.1	3	6	0.3	3.6	0.91
Openness	4.0	1.2	2	6	0.2	3.4	0.93
Conscientiousness	4.5	1.0	3	6	0.2	3.3	0.94
Emotion Regulation	4.2	1.1	3	6	0.3	3.5	0.90
Stress Management	4.0	1.2	2	6	0.2	3.4	0.93
Problem Solving	4.5	1.0	3	6	0.2	3.3	0.94
Decision Making	4.2	1.1	3	6	0.3	3.6	0.91
Goal Setting	4.0	1.2	2	6	0.2	3.4	0.93
Time Management	4.5	1.0	3	6	0.2	3.3	0.94
Organization	4.2	1.1	3	6	0.3	3.5	0.90
Productivity	4.0	1.2	2	6	0.2	3.4	0.93
Efficiency	4.5	1.0	3	6	0.2	3.3	0.94
Effectiveness	4.2	1.1	3	6	0.3	3.6	0.91
Adaptability	4.0	1.2	2	6	0.2	3.4	0.93
Flexibility	4.5	1.0	3	6	0.2	3.3	0.94
Resilience	4.2	1.1	3	6	0.3	3.5	0.90
Optimism	4.0	1.2	2	6	0.2	3.4	0.93
Gratitude	4.5	1.0	3	6	0.2	3.3	0.94
Forgiveness	4.2	1.1	3	6	0.3	3.6	0.91
Empathy	4.0	1.2	2	6	0.2	3.4	0.93
Compassion	4.5	1.0	3	6	0.2	3.3	0.94
Kindness	4.2	1.1	3	6	0.3	3.5	0.90
Patience	4.0	1.2	2	6	0.2	3.4	0.93
Humility	4.5	1.0	3	6	0.2	3.3	0.94
Generosity							

GGAAGTCCACCGGGAGCTTTGGATGCCAAAGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACACAGCCTCAGATACTGGGGACTTTAC
 AGTCCACAGAACCCTCCTCCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
 AGCTCATTTGCAGACAAAGGCAAGTCCTTTTCTCTCTCTTTGGGCTTATCTCTGGCG
 GGCGCGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTAC
 CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG
 TTTCCAGAGGGAAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTGTGTGCTAAAT
 GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT
 GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
 ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG
 ACTACGTTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAAAATATTGAGAACTA
 TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAACGCAGTGATGGCAGGAAAT
 ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTAAACA
 CTCACAGCACTGGATGGTGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
 CCTGGATGTCAACGATAATGCCCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
 AGGACAGTCCGGTAGGCTTCTGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
 AACGGAGAGATTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
 CAATCCCTTGACAGGAGAAATTGAACAAAAAACAACCTCGATTTCGAAAACTTCAGTCCT
 ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTCTGGAAAATGCACCGTTCTGATT
 CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
 ACCTGAGAACCGCGCTGAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTGAGGAG
 AAAATGGGAAAATTAGTTGCTCCATTGAGGAGGATCTACCCTTCTCTGAAATCCGCGGAA
 AACTTTTACACCCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
 CACTATCACTGTCTACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
 TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCTGTTCGTC
 CGCGAGAACAACAGCCCCGCCCTGACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG
 CACCAACGCCCAGGTCACCTACTCGCTGCCGCCCCAGGACCCGCACCTGCCCTCACAT
 CCTGGTCTCCATCAACGCGGACAACGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG
 GCCCTGCAGGGGTTCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG
 CGAGGCGCTGGTGCGCGTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC
 CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC
 CTGGTGACCAAGGTGGTGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTGCTACCA
 GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA
 CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC
 AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGACGGCTTCTC
 CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGACCCAGGCCAGGCCGACTTGCTCACCG
 TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT
 GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTTGGTGCCCGA
 GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCCAGGACCCCTATCCAGAGCTACC
 AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCTGAAGCCGATT
 ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA
 TAACTTTGGGTTCAATATTGAGTGACCATAGTTGACTTTTACATTCCATAGGTATTTTATTT
 TGTGGCATTTCCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT
 TTAATCTTGATTTTCTCATGTTCTTTCTCCCTTGTTTTAAAGTGAACATTTACCTTTATT
 CCTGGTTCTT

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLFESPFQELQV
IDINDHSPVFLDKQMLVKVSESSPPGTTFFPLKNAEDLDVGQNNIENYIIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAEELRLTLTALDGGSPPRSGTAQVYIEVLVDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVAVDGDGSGQNAWLSYQLLKATELGFLGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYPPLPEAAPTQAA
ADLLTVYLVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPFPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
CACTTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC
GAACACTGGAAACACTGAAAATCTTCATTTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACTCAAGCCGACCAAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGTATTTTCCTTATTCTTTTAAATTAGTTTTATTATGTATGCTACCATTTCGAA
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPVRMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTTCGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLFLLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCA¹ACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCCTGGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAAGTGACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTAGAAATATTCAAACCTAATA
AAATCATGAATATTTTAA

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGLLLLFLASHCCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLD ETIQPCHSLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSE RDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQG GELVITSVKRWQKGQREFKRISR SIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

FIGURE 168

GTGGAGGCCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGGC
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTGGAACCTCTGGGCGTCCTTGTGGCCAATGTGCT
GTCCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCCCG
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAACTTCCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG
CCTGCGTGCCCTTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA
GTGTTCTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTTGGGGCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQIQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGLIMLAMTALTVRRSEPSLSTCQQGEDPLDWTVSLLL MAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

[illegible]

GTCCACATCTCTGCTCAACTGGGTGAGTCCCTCTTAGACACAGCTCTTGTTCATCTATTGTCTGAAGTGGACCAAC
TAGTTCCCCAGTAGGGGGTCTCCCCCTGGCAATTCTTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGGCCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT
TCTGAATCTAGCCCACTTGGCGGTAAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGGATGTGTCAGGAGGTGACCACTCTCAGGTTGAAATACCAAGTGTCTCAGAGGAAGTGCC
ATCTGGTACAGTGTCTCGGGAAGCTGTCCAGGAATCGGCCCGGAGGAGGCGAGGCAAGCTGGGGCCCGCTT
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGTCTCAGCAGCAGGCGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCTGCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT
GGCTCTGATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGG
GCTGGAATCTCTGAGAGCGCCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC
TAACAACTGCACCACTACACTCTGTCTCCAGTGAGCACTTTGCTTGGATGTCATTGTGGGCCCTTGATGAGAC
CAAACATGCAACTCATAGTGGTGAAGAGCTGGACAGGGAATCCATTGCTATTTTGTATCTGGTGTAACTGCT
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAGCTTTGGTCAAGGTCAACGTCTTGGACTCCGATGACAATG
CCCTGCGTTTGTCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT
GACCGCCACAGACCTTGACCAAGGCCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCCTCCAGAGGT
GCTGGACACCTTCTGATTTGATGGCAAGACAGGCCAGGTCATTCTGCGTTCGACCTTAGACTATGAAAAGAACCC
TGCTACAGGTTGAGTGTTCAGGCAAGGGACCTGGTCCCAATCTATCCAGCCATTGCAAGTTCTCATCAA
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTTCATGTTGGGCTCCAGCCACTCTGGTGTGCAAGC
TCTTCCCAAGGACAGTTTTATTGCTCTTGTCTATGGCAGATGACTTGGATTAGGACACAATGGTTTGTGCTCAAGC
CTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC
CACACTGGACAGAGAGCAGTGGCCCCAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAGAAAACAGCTCAGCATCTCAGTACATCAACGACAATGCACCTGTGTTTGGAGAAAACAGGTATGA
AGTCTCCACGCGGGAACAACTTACCTCTCTTCACTTATTACCATCAAGGCTCATGATGCAGACTTTGGGCAT
TAATGGAAAAGTCTCATAACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGGTCACTGAACATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG
GCAACCCATGCTTGCATCCAGTGTCTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT
CCAGCTGTGCTCAGCGATGGAAGGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGGC
CATCGAGACTCCCAATGGCTTGGGCCAGCGGCACTGACACACCTCCACTGCGCCACTCAGCTCCCCGGCCATT
CCTTTTGGACAACCAATTGTGGCAAGAGATGCAAGTCTGGGGCAAAATGGAGAGCCCTTACAGCATCCGCAATGG
AAATGAAGCCCACCTCTTCATCTCAACCCTCATAACGGGGCAGCTGTTTGTCAATGTCAACCAATGCCACAGCCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCACTGTTTGTACCAGTGTGGACACCTGAGGGACTCAGCCCGCAAGCTTGGGGCTTGGAGCATGTGAT
GATGCGGTGATCTGCCTGGCTGCTACTGTTGGGCATCTTGGGTGATCTGGCTTGTGTTTGTGATGTCATCTGCGG
GACAGAAAAGAAGGACAACAGGGGCTCAACTGTCTGGGAGGCGGAGTCCACCTACCCGACAGCCCAAGAGGCC
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGCTCAGGAGGTGAGCCTTGTGAAGT
CGGGCAGTCCCAAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCTGACAGGCCCTT
CCACCTCACCCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGT
GCTGCAAGACACGGTCAACCTCTTTTCAACCATCCAGGCTCAGAGGAATGCTTCCCGGGAGAACCTGAACCTTCC
GAGCCCCAGCCTGCCACAGGCCAGCCAGTTCAGGCCCTGTGAAGTTGTCAGGCAGCCCCACAGGGAGGCTGGC
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACAGCCTCTCTGCAACCTTGAGACGGCAGCGACATCT
CAATGGCAAAGTGTCCCCTGAGAAAGAATCAGGGCCCCGTGAGATCTGCGGAGCCTGGTCCGGCTGTCTGTGGC
TGCCTTTCGCGGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCTCTCTGTTTTCAGCAAATCTCCAGCTGCT
GTCCTTGTGCTGATCAGGGCCAACTTCAGGCCCAAACCAACCAAGGAGGAAATAAGTACTTGGCCAAGCCAGGAGG
CAGCAGGAGTGAATCCGAGACAGATGGCCCAAGTGCACAGGCTGGAGGCCAGACAGACTGTCAAGTCTGCTGGACCC
AGGGCCTTTGGATCCTGGAAGAGGACCTCTCTGTGAAGCAACTGTGTAAGAGAGAGCTGTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCCTGACCCGGCTGATGGCGAGACTCTTTTGGCCCTCAC
CACCAACTACCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTTCGG
CAAGGCAGAGGCCACAGAGCTGAGCCCAACAGGCACAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGTTGGAACACGCGCTCCAGCATGCCCGTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACCAAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGGACTGAGGGCAAGAGCAGAGGACGACGACGAGCAGCTGCTGTAACATCTCAGACGCCT
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAATCTTTGTAACCTCAGTAGCTAG
CGGCGGCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC
TGACCAAAGCAGCCCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGT
TCCTGTGCAAAACATATGTGGAGCACAAAGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG
AAAGGTGGCCTTCTTGGGTAGCAGGAGTCAGGGGCTGTACCCTGGGGGTGCCAGGAATGCTCTCTGACCTAT
CAATAAAGGAAAAGCAGTAAAAAAGGAAAAAAGGAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEELEISESASLRTRIPLDRALDPDTGPNLTHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESS
LALEIQEDAAPGTTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPPIPAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQRSLNVEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTT
IVARDADSGANGEPLYsirngNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHQKAD IHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCLOAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLPEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGGS
RSAIPD TDGPSARAGGQTDPEQEGLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDPGGKTGTEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTTCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGA CTCTC
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCTCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAATCACTGAAGTCTTGGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTCACTTCATAGCATACTCCTTCCCCGTGAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTTATTGCAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLEFSCLLWLTFMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

Figure 174

[illegible]

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT
TTTTTCATGCGCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCCTC

FIGURE 176

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT
TGGCTCCCTGCTCGTCGAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCACAA
GGAGGGCGAGCCAGGCAGCCTCTTCCGGCTTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCGAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTG
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAGTGTTGGGAGTCACTGTTGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG
TCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGTCTGGTGGCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA
CAAGGGTGTGTGCTCATCTGCGCAAGGACAGCGCCAGTGCCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGCTTTGGCTACTCACTGGCTGTGGTGGCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGTGGCTGGCCCCCTTTGATGGTGGTGGGAAAGTCTTCACTACCA
TGGGAGCAGCCTGGGGGTTGTGCGCAAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCCGAGGCTCCGGGGCCAGGT
TCCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGT
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC
CCCCATCCTCAATGCCCACAGCCCAGCACCCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCGAAC
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGGTGGGCGAGCCAGTCAATGGCCTGGAGCTGAT
GGTCAACCAACCTGCCATCGGACCCAGCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCATGAAGAGAGGTGCCAGGTCACTTCTACCTCAT
CCTTACCACTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGCTGCTGTTGGCCAGCATCAGTGAGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCAATTGAGCTGCCATGTCCATTGAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTCTGGTGTGGTGGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTGCCTCAGAACCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGA
GCTGGAGCCACTTGAGCAGCAGGAGCCTGGTGGAGCGGAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGC
TGAGAAGAAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAAGTGTGTGGTGTTCAGCTGCCACTCTA
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCAGAGTGAAGTCCCTCATAAAGAACTTGATGCTCCGAGA
TGCCTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGT
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGCTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT
CAAACGGGCGAAGCACCCCCAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTTCGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAATGGGGCAGCCCCCGGCGGGAGGGGCCGGATGCACA
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCTAGGTTCC
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGTGGTGTGCGCATCAAGATTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC
TCCTCCACCCAACTTCCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGTCTGTATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCCATCACCTGT
GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCCTTAACCTAGAGGGTCCGGGAGGAGGTTGTGTCACTGA
CTCAGGTGCTCCTTCTCTAGTTTCCCCTCTCATCTGACCTTAGTTTGTGCTGCCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTATTAAAAAATATTTGAGAACAAAAA

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMOKESKENQWL
GVSVRSQGPQGGKIVTCAHRYEARQQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGEWKFC
RPGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ
SPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAGAPFDGDGKVFIYHGSSLGVVAKPSQVLE
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQ PSTQRAEIHFLKQCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSN
ENASHVECELGNPMKRG AQVTFYLILSTSGIS IETTELEV ELLLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVT VSNQGQSLRTLGS AFLNIM
WPHEIANGKWL LYPMQVELEGGQGPQKGLCS PRPNILHLDVDSRDRRRRRELEPPEQQEPGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANC VVFSCLY SFDRAAVLHVWGRLWNSTFLEEY
SAVKSLEVI VRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYH AVKIPREDRQQFKEEKTGTILRN NWGSPRREGP
DAHPI LAADGHPELGP DGHPPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACCTTGGAGTCCAGGAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTC AAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC
CATGATGTATACATTTGATTTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCTTACACAAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTACGAGAACAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTTGAAAG
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSONKKTLLRPERSRFDTSILPI
CKDSLGMFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQODPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSGVQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDDDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 179

FIGURE 180

CAGACTCCAGATTTCCCTGTCAACACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
 CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGCGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTTCTGGCC
 GCTCTGCCTCCGGTGTCTGCTGCCCTGGGGCGGCCGGCTTACACCTTCCCTCGATAGCGACTTACCTTTTACCCTT
 CCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCCCTGAAGGCCCTCGCTGGAGATCGAGTACCAAGTTTGA
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCCAAAACCTTAGTTTTTTGAACAAAAGAAA
 TCAGATGGAGTTTACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTAGCACCATT
 TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG
 AAATATATTACTGGCACAGATATATTGGATATGAAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
 AGACTAAGCAAAAGTGGGCACATACAAATTTCTGCTTAGAGCATTTGAAGCTCGTGATCGAAACATACAAGAAAGC
 AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAAGCTTAAACTCCAAACTAGAGTACGTAACATTGAAA
 AATGAGGCATAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAATATTTTGAGATATA
 AAAGTAGGAAAACAGGTATAATTTTAAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
 TTGTACTTAAAGTGTGTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT
 TTTCTTAACCTTTGAAAAATTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC
 AGTCTGTTTTTAAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT
 TCAGTTTTTAAGTTATAAAATCACTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA
 CTTTTCTCTATTACATATGCATCTCTCCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG
 AGATTTTTTATAACCAAATACATTTTCACTGTAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
 CAAAAGCTGACATTTTTCACGATCTTAAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
 AAATGAAGAATATAGTTTAAAGCTTCTCCTCCATAGGGACACATTTTCTCTAACCCCTTAAGTGTAGGA
 TTTTAAATTAAGTGTGAGGTAAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
 TAATCATGTTATGTTAATTTTAAACATGATTGCTGACTTGGATAAATTCATTATTACCAGCAGTTATGAAGGAAATA
 TTGCTAAAATGATCTGGGCCTACCATAAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA
 AGAATTTAGAAAAACTTGAGAAAACCTAATCCAAAATAAATTCACCTAAGTAGAACTATAAATAAATATCTAGA
 ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
 AAACCTTTGGCTGTAGGTTTTTATTTTCTACAAGAATCTGGTTTGAATTTATTTTGTAAAGCAGGTACATTTTATA
 AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGACATATTTATTAATAAATTTTATTATAACAACCTTTTAT
 TAAATGGCCTTTCTGAACACTTTTATTTATTTGATGTTGAAGTAAGGATTAGAAAACATAGACTCCCAAGTTTTTAA
 CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC
 TCAAGTACTAGTAATTTAAGTTCATCATGAATGAACATAATTTTAAAGTTATGCCCATTATATAACGTTGTTTTAT
 GACTACATTTGTGAGTTAGAAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT
 CTTGATGAGCAATAATGATAACAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
 TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAATAAGGTAATGCCGTAT
 ATGATCAATTACCTTAATTTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA
 AGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTGGCGTGTAAATTTGCAATGAGAAGCAAATTTACA
 GTACCATAACTAATAAGCAGGTTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTTCTA
 CCTCTCCTGTATGGCTGTACTGTACTCTCTGACTCCTTACCTAACCAATGAATTTGTTACATAATCTTCT
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTTCAGTAACTTCTTACCATATAAAAACGATAATTGCTT
 TATTTGGAAGAATTTAGGAATACTAAGGCAATTTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
 CATAACCAAAAAAGCAAACTGTAAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT
 CATATGCTTTTTTTTAAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTT
 AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTT
 CATAATGTAGCAGTTACCGTGTTCACCTCACACTAAGGCCCTAGAGTTTGTCTGATATGCATTTGGATGATTAAT
 GTTATGCTGTTCTTTTCACTGTGAATGTCAAGACATGGAGGGTGTGTAATTTTATGGTAAAATTAATCCTTCTTA
 CACATAATGGTGTCTTAAATTTGACAAAAAATGAGCACTTACAATTTGTATGTCTCCTCAAATGAAGATTTCTTTAT
 GTGAAATTTTAAAGACATTGATTCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTG
 CTCAAAGTCTTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA
 AAATTATCAAAGGAAAA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

FIGURE 181

FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC
TTCTTTTTCTTTTTCTTCACCTTCATTTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

[illegible]

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACAGGAGTGT
CGGACTGTGTCAACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCTGTCTCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

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[illegible]

CTGCAGTCTCAGGACTCTGGGACCCGACAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGGCTCTCGGCGGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTTAGTTAAGCAT
TCCAATAACACCTTCCAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG
CTGGGCCCGTCCGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA
AGTATTAGAAATGAGCTGAAGACCATTCACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCT
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
TTAAATCAGAACTTGCATAAGAAAAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTTGG
AGTGTCCAAAACCTGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTTGGCATTGAAGTTACATCCTGATAA
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA
AGGAGGAGATTGTTTTGACTTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTTCTCAACTCATTGGATGCTAA
AGAAATATATTTGGAAGTAATACATAATCTTCAGATTTTGAAGTACTTTTCGGCAACACACTAGAGGATCGTTT
GGCTCATCATCGGTGGCTGTTATTTTTCTATTTTGGAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAAT
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTCTTCTCTGCACCAGACATCTGTAGTAA
TCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAGAAATATGAAATTCATCATGGAAA
GAAGATTCTATATGATATACTTGCCTTTGCCAAGAAAGTGTGAATCTCATGTTACCACGCTTGGACCTCAAAA
TTTTCTGCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCTTGGTGTCCACCATGTCCAGCTTTACT
ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTCATGA
GGGACTCTGTAACATGTATAACATTCAAGCTTATCCAACAACAGTGGTATTCAACCAAGTCCAACATTTCATGAGTA
TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
ATCCACCACCTTCAACGAAGTAGTTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG
GTGTCATCCTTGGCAAGTCTTAATGCCAAGTGGAAAGAAATGGCCCGACATTAAGTGGATGATCAACGTGGG
CAGTATAGATTGCCAACAGTATCATTTCTTTTTGTGCCCAGGAAACGTTCAAAGATACCCTGAGATAAGATTTTT
TCCCCCAAATCAAATAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATCCCTGAGAAT
CTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGTGAAAAAGTTCTACAAGG
GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCT
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA
AGCTGGGATCAGGGCTTATCCAAGTGTAAAGTTTATTTCTACGAAAGAGCAAGAGAAAATTTTCAAGAAGAGCA
GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAATAATTTGGAAGTCTCCGAAATCAAGGCAA
GAGGAATAAGGATGAAGTTGATAATGTTGAAGATGAAGAAAAGTTTAAAAGAAATTCGACAGATGACATCAG
AAGACACCTATTTAGAAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
GAATTATCTACAGCACTGGTGTAAAGAAGGGTCTGCAACTTTTTCTGTAAAGGGCCGGTTTTATAAATATTTTA
GACTTTGCAAGCTATAATATATGTTTACACATGAGAACAAGAAATAGAGTCATCATGTATTCTTTGTTATTTGCT
TTTAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTTCAGTCCATG
GACCATAGATTGCTGTCCCTCGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAC
TAGTTTTTTGGTCACTTGTTCTCTCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTTAAACACCCAT
GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTTATGAGGAGATTTCTTATTGTTTTCTTCTCTCTCA
AAGGTTGAAAAAATGCTTTTAATTTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGCTGATCATCCAGGAAAACCTGAGGGAAAAAATTA
TAGCAATTAAGTGGCATTTGATAGATATCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
TGTGTTTCATGATTTTCTGAAATTTGCTTTTCATAGAAATTTTCCACTGATAGTTGATTTTTTGGGCATCTAATAT
TTACATATTTGCCCTTCTGAAGTTTGTGTTTACCTGTATCCTTTATTTACATTGGGTTTTTTCTTTTCATAGTTTGG
TTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAATTAATTTACAGGTTGTTTTTACTGTAGCTTAT
AATGATATCTGATTTATTTCCAGTTACTAGTTTACTGTGAGGGCTGCCTTTTTTCAGATAAATATTGACATAATA
ACTGAAGTTATTTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGA
CTCAAAGAATCACAAATTTGTGAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGTAAAAAT
CCAATCAGTCAAAGAGGTCAATGAATTAAGGCTTGCACCTTTTTTCAAAAAAAAAAAAAAAAAA

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSL LGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGL EDNQGGQYESWNYRYDFGI
YDDDPEIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAF AAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYVFQP
SLAVFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS
AEQILEFIEDLMNP SVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTD LTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAP EPELLARMIKGKVKAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLET LRNQGKRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA
GTCGTTGGTGAAGTTTTTTCATTCCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTGGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTTACCA
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTTCTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATTGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTTTT
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCTGTTTTCTCAAGAAATTTTACGTAGTTTTTTCATAGGTCTGTTTTTCCTT
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGA
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT
TCATTAGCCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCTCCCTTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESIVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDVTIVVNNAGTV
YPADLLSTKDDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRSIID
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCACAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCCGGGG
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCTTCT
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCCCGGGCCGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCGAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCTTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELTA
DSDVDEFLLDKFLSAGVKQSDLPRKETEQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFP TKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSL LHRGAPYRDPLRIPREHVHNASAHLT FNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELNEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLD EDAAQLLQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLF GYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 195

TCGGGCCAGAATTCGGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTTCGTGACCGGGGGCGGGCGGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCCGCATGGGCCAGCCCGCTGAGGTGGGGCTGCGGCAGTGTTCTTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCCGATATCCCTTCCTTGATTTCTCTCATT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQRPETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

[illegible]

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY

ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCL

GCVNPFTMQEDRSMVSVFVSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

Protein: 59294

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTGAGAATGGGAGGCTTTTGCAGAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG
GCCGCTTCTTTGTCACCACTCTCCCAGCATTFTTTTCATGCAAAGGATGGGATATTCCGCCGT
TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACCTATTTTACAGTGACTCTTGGAATT
CCTGCTTGGTGTCTTATGTGTTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAAATGTTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAACAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC
TGTAGATTTAATGATGCGTTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTTGTACCAAATCCTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAATCAGGATATAGAAAAACAACGTAAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTTTCTGTGTAAAGTATTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAAA
GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQT DSEWEAF AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLQDAEEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

the "seqdb2"

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTAGGGGCTCTCAAGAAACAATGGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTAGCATGTCCT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTATAGTAAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTACAGTGTGAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGCGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTTTGGAGATAGGGTCT
CACTTTGTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCGAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTCAT
TTCAATAAAAAAAACTCTTATCAAAAAA

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

[illegible][illegible]

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLIQTTLLFLLSLLFLVQGAHGRGHREDFRSCQRNQTHRSSLHYKPTPDLRISIENSE
EALTIVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QESLAQGPPLLATSVTSWWSPQNISLPSAASFSTFSFHSPPHTAAHNASVDMCELKRDQLL
SQFLKHPQKASRRPSAAPASQQLOSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTLQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTFPVLTTFQHQLOPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVDVAVHKHYLSLLSYVGCVVSAALCLVTIAAYLCSRVPPLPC
RRKPRDYTIKVHNNLLAVFLLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGLIFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATACCAACCTGGGCCTCTTCAGCCT
GGTGTTCCTGTTCAACATGG

Figure 205

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCTAGGTCCAGGTTTTGCTTTGA
TCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAGAGAGAC
TCGGGAGTGCCTGCTTCCAAAGTGCCCGCGTGGAGTGAGCTCTCACCCAGTCCAGCCAAATGAGCCTCTTCGGGC
TTCTCTGCTGACATCTGCCCTGGCCGCGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTC
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTTACGTTTGTATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT
TCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCTTTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAAGACCTTATTTCGATATCTTGAACCAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTTGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTTCT
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG
GTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCTTTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCAAAATCACTACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCAATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGGAGAGGAGGCTTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAGAAAATTAAATGTTGTAT
TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC
GATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCTGGGCCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGCTCATATTCACAT
ATGTAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAACCTTGT
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAATAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
TTTCATGTGTACATTTTTATATTTCTCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT
ATTTTTTACCAAAGGTATTTAATATTTCTTTTATGACAACCTTAGATCAACTATTTTTTAGCTTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTTGTTGCTCTGACAAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAATAATTAAATTAATCATATCTTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA
AAGTAGACATTGAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGTGTGCTGTGCAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAAATACATGGATATTTTTATGTACA
GAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCAATTTAAAAAGAAAATCAGTAAAATATTTTGTCTGT
AAAATGCTTAATATNGTGCCTAGGTATGTGGTGAATTTTGAATCAAAAATGTATTGAATCATCAATAAAAAGA
ATGTGGCTATTTTGGGAGAAAAATAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

FIGURE 206

FIGURE 207

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKSRVVDLNNLLTEEVRLY
SCTPRNFVSISIREELKRDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

Signal sequence:

amino acids 1-14

protein sequence

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCATTTTGGGAAGA
AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATCTTATCCTTTTAAACATAATCCTAATTTCC
AACTCCTTGGGGCTAGATGGTTTCCCTAAAACCTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTTCCACGAACACCACGAACCTCACCCCTC
ACCATTAACCACATACCAGACATCTCCCCAGCGTCCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCA
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAC
TTAGTGGACTCACTATTAAAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCCG
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
AACATAGAAATACTCTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTGTATGTTTCATATTCAATAGAGAAA
GATGCCTTCTTAACTTGACAAAGTTAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAAATAAC
CTCAACCAATTACAAATTCCTTGACCTAAGTGGAATGGCCCTCGTTGTTATAATGCCCAATTCCTTGTGCGCCG
TGTAATAATAATTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAGTTTACGTCTA
CACAGTAACCTCTTTCAGCATGTGCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACGGATCTGTCC
CAAACTTCTTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAATTGGATCTG
TCTTTCAATTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG
AAAATCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATTGCTAACCTCAGCATGTTTAAACAAATTTAAAGA
CTGAAAGTCATAGATCTTTTCACTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAA
GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCCTGGAACAATTACATATTTTCAAGATATGATAAGTATGCA
AGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTTATGTCGTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC
TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTTCTTCTCAAATGCCTG
AATCTGTGAGGAAATCTCATTAGCCAAACTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTG
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCAAACTGGAAGTTCTGGAT
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACCAAGAACCTAAAGGTT
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTAAG
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAATCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGT
ATGCCTCCAAATCTAAGAATCTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
CTAAGAACCTGGAACCTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTATCCAACCTGTTCC
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTC
ACAATCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTTGTCTGGTGG
GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
TCTGTATCTCTCTTTCTCATGGTGTGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA
CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACTGAAAATTTAAGATAGCATTTTAC
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAG
TCCAAGTTCTCCAGCTCCGGAAGGGCTCTGTGGGAGTTCTGTCTTGAGTGGCCAACAACCCGCAAGCTCAC
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLOHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDTGNTFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLNFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWVWNHTEVTIP
YLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAAACAGAAACATGGAACATGTTCTTC
AGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTCCTGTGAGTTATGCGCCGAAGAAAAATTTTCTA
GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGACAGAGTGACGAATCGTCGACTACAGGAAG
TTCCCCAAACGGTGGGCAAATATGTGACAGAACTAGACCTGTCTGATAATTTATCACACATAACGAATGAAT
CATTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC
CCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCTCAACCTAAAAAACCTAAGGGAGTTACTGC
TTGAAGACAACAGTTACCCCAAATACCTCTGCTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTTCAAAACA
ATATATACAACATAACTAAAGAGGGCATTTCAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAGTGT
ATTTTAACAAAGTTTGGGAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT
CACTATCTTTCAATTTCTTTTACACGTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA
CCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAAATTTAACATTACTAGATTTAAGCGGGAAT
GTCCGAGGTGCTTCAATGCCCATTTCCATGCGTGCCTTGTGATGGTGGTGTCTCAATTAATATAGATCGTTTTG
CTTTTCAAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGT
TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT
TTTTAACGATGCTGCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCATA
TTAATATTTCCAGAAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAAC
TCAGAGAAGATGATTTCCAGCCCTGATGCAGCTTCCAAACTTATCGACTATCAACTTGGGTATTAAATTTTATTA
AGCAAATCGATTTCAAACCTTTTCCAAATTTCTCCAATCTGGAATTTATTTACTTGTGAGAAAAAGAAATATCAC
CGTTGGTAAAAGATACCCGGCAGAGTTATGCAATAGTTCTCTTTTCAACGTATATCCGGAACGACGCTCAA
CAGATTTTGAATTTGACCCACATTCGAACCTTTTATCATTTTCAACCGTCTCTTTAATAAAGCCACAATGTGCTGCTT
ATGGAAGGCTTAGATTTAAGCCTCAACAGTATTTTCTTATTGGGCCAAACCAATTTGAAAAATCTTCTGACA
TTGCCTGTTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAACCTGAATTTTCAAGCATTCTCATG
TCAAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTTGCTCGACTGG
AAGTTCTAGATCTCAGCTATAATTCACACTATTTTCAAGATAGCAGGCGTAACACATCATCTAGAATTTATTCAA
ATTTCAAAATCTAAAAGTTTAAACTTGAGCCACAACAATTTTATACTTTAACAGATAAGTATAACCTGGAAA
GCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCTTGACATTTTGTGGAATGATGATGACAACAGGTATA
TCTCCATTTTCAAAGGTCTCAAGAACTGACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATG
AAGCATTCCTTAAATTTGCCAGCGAGTCTCACTGAACATATAAATGATAATATGTTAAAGTTTTTAACTGGA
CATTACTCCAGCAGTTTCTCTGCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGATAGG
TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCACCTACCTCTGGCTTTC
TTTCTGAAGTCAGTAGTCTGAAGCACTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG
AACTAAGACCACCACCAATTTATCTATGTTGGAACCTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAG
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATCCCAGACTGGTAGATGTCAATTTGTGCCAGTCCCTG
GGGATCAAAGAGGGGAAGAGTATTTGTGAGTCTGGAGCTAACAACCTTGTGTTTCAAGATGTCAGTGCAGTGATTTAT
TTTTCTTCAAGTTCTTTTATCACCCATATGTTTATGTTGGCTGCCCTGGCTCACCATTGTTTTTACTGGGATGTTT
GGTTTATATATAATGTTGTTTATGCTAAGGTAAAAGGCTACAGGTCTCTTTCCACATCCCAAACCTTCTATGATG
CTTACATTTCTTATGACACCAAGATGCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAG
AGAGCCGAGACAAAAACGTTCTCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC
TCATGCAGAGCATCAACCAAGCAAGAAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAGCTGGAACTTTA
AAACAGCTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATGTGATTATTTATCTGCTGGAGC
CAGTGTACAGCATTTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACA
ACCCGAAGGCAGAAAGCTTGTGTTTGGCAAACTCTGAGAAATGTGGTCTTGACTGAAAATGATTACCGGTATAACA
ATATGTATGTCGATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTGCGCCATAATAAAGATGCAAAAG
GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTTATCCCAAACTTAGTGGTTTAAAAACAACA
TTTGTGCGCCACAGTTTGTGAGGGTCAAGAGTCCAGGCCAGCATAACTGGGTCTCTGCTCAGGGTGTCTCAG
AGGCTGCAATGTAGGTGTTTACCAGAGACATAGGCATCACTGGGGTCACTCATGTGGTTGTTTTCTGGATTCA
ATCTCTCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCAAGGCAGCTTGCTTC
ATCAGAGCTAGCAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAATCAAAAAAGTGAT
ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCACCAGCTCCATGGGAGTGACCACC
TCAGTCCAGGGAAAAACAGCTGAAGACCAAGATGGTGAAGTCTGATTGCTTCACTGGTTCATCAACTATTTTCCCT
TGACTGCTGTCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC
ATCTTAGCAGTTGACCTAACACATCTTCTTTCAATATCTAAGAACTTTTGGCACTGTGACTAATGGTCTTAATA
TTAAGCTGTTGTTTATATTTATCATATATCTATGGCTACATGTTTATATTTATGCTGTGGTTGCGTTTCTAT
TTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTATAGTCCATTTAAGAACTGAGATGG
ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAGTATGACGCTAAATTCGAAGCTTTTGGTCTATA
TTGTTAATTGCCATTGCTGTAAATCTTAAATGAATGAATAAAAAATGTTTCATTTTACAAAAA

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQNDSVIAECSNRRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFSLNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFQNLTLQLRYLNLSSLSLRKINAAWFKNM
PHLKVLDLEFNVLVGEIVSGAFLTMLPRLEILDLSFNYIKGSPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSLNLEIIYLSNRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRDLNRLKHIPNEAFLNLPASLTTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDLS
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPGLAIID
NLMQSINQSKKTVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGFLWQTLRNVVLTENDSRYNNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCATCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTTCCTG
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTGA
AAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTATGTCAGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPrVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

protein sequence

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCACGGGGGCCCCGGGGAGGGGAAC TGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCT
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCG
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA
CTCGTGA CTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCTCCTCCCCTTCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCTCAGCTGAGGGAAGGTACGAGCTCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACATAAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSDGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

Protein sequence

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGGGAGGGGACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCTCCTGGAGGAGCAGCT
GGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCTCCTCCCCTTCTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCTGGCTACC
CCCACCCTGGCTACCCCAACGGCATCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

1-19

FIGURE 218

GGTTGCCACAGCTGGTTTtagggccccgaccactggggcccccttgctcaggaggagacagcctccccggccccgggag
GACAAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCTGGGACGGTCCGTTTCTCGCCGTGAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTcaggccggctcccccttcttgggtctcccttctcccgctgggccccgtttatcgggagg
AGATTGTCTTCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTCTTCTCTCGTGTAAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATCA
TGTCTGTGATGGTGGTGAGAAAGGTGACACGGAAATGGGAGAACTCCAGGCAGGAACACCTTTTGCTGTG
ATGSCCGCGTCATGATGGCCCCGGCAAAAGGGCATTCTTCTACCTGACCCTTTTCTCATCCTGGGGACATGTACAC
TCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTGTTTcagctgtctcctgccatccctgtatttgctgccatgctct
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTcagtgacctggagtgattcctcgggCGCTACCAGATG
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA
TCAAGAATTTCCAGATAAACCAACCAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC
GGCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG
TTGGAAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGCTTCGCCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGAGACATTGAAAGAACTCTGGAAGT
TCTAGAAGTCCTCATTTGCTTCTTACACTCTGGTCCGTCTGGGACTGACTGGATTTCATACCTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCCAGAGAACCTGAACCTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTT
TAATTAGGGCTATGAGAGATTTcaggtgagaagTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTCTTCTGCTGCAAGCTTTTTTAAATTTCTGAAC
CAAGGCAGTGGCAGAAGATGTcagtcacctctgataactggaaaaatgggtctcttgggccccctggcactggttct
CCATGGCCTCAGCCACAGGGTCCCCCTTGGACCCCCCTCTCTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCAC
TGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCCAAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTACTCCTGCTCCCATTAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAAGTTCTTCCATTAAAGCCT
CGGCTGAGTGAGGGAAAGCCCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCAGAGCCACTT
CACCTTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTcagggaaagaagATTATGT
ATTATATGTGGCTATATTTCTAGAGCACTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAAACTGTGTCTAATGCA

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGNRYRYFYL
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLETLPKTPGTVLEVLIFFTLWSVVGLTGFHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAKE

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

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FIGURE 220

AAAACCCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGAATTGTGTTGGAAAGAGGAATA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

CCCTGTTGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT

FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCAACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAAGAAGAAAAAGAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTCT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACA
TTTCAGAAAGCCAAGGTTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCCTGGCTCCAAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCCACAGAGTGCCCCCAGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

FIGURE 222

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMD NVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISP KAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIF FNVSEHDYGN YTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

Signal peptide:

amino acids 1-28

FORM 5304-100

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

Sequence

FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCACAGCACCTGCCTTACA
GAGGCTGCAATTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGA AAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTCAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAACGCTTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCACTGCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTGCCCCAGGACCAGCGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTCAAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGTAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCAGCCGAGACCACTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCCAACCACCCCAAGGCCCTGAACCTTCGGTGGCATC
GGTGTGGTCAATGGGCCATGAGTTGACGCATGCCCTTGTATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAAACATTACTGACAACGGGGGGCTGAAG
GCTGCCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGCTCGGTCCGCAACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG
CACTTCGGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCCTCCTCAATCACCACATTG
TGCCTCTGCTTTGGGGGTGCCCTCCAGCAGAGCCCCACCATTCACTGTGACATCTTCCGTGTACCCCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCTCATAGGAAGGAGTCTGCC

FIGURE 225

MNVALQELGAGSNVGFQKGRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRD LIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDY YLNRTANEKVL TAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQ LANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEK LLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLP TKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNP GQLCEVW

Type II Transmembrane domain:

amino acids 32-57

protein : 980600

FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCCTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTCCGA
GGAACCCCCTGCCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAAACTGCCCCCT
CCTTTCTTTCTTCTTTTCTTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCCTTCCTTCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCCTGAAGAGATTGCATTTGAGCCAGGTCTCTAG

FIGURE 228

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCTT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCTATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCCCTGTGCTCCTTGTGCCACTGCTCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

FIGURE 228: SEQUENCE

FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA
GGAGGGGAGGCAAAAACACCGAAAAACAAAAAGAGAGAAACAACACCCAACTGGGGTGG
GGGGAAGAAAGAAAGAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG
TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG
CTGTTGGTGCAGGGTGCTTGTGCTCGAACCAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG
CTGCCTGCTACCCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCCTGGGCGGCCGTGG
ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT
TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTCGCGGAGGTGATAAGTGGTCAGT
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG
TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTTCAGACTCAACATACACCCAGAACA
ATGCAGGTGCATCTAAGTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACCAGAGCCTTCCA
TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT
TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCAGGAAAATGCTGTGTCATT
CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTAGGAAATTAAAT
CTGGCACCGTGACCCCGGACGAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT
CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT
TCAAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA
ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCT
CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTCTCCTGCTGGTACCT
TGTGTTGACACTGTCCTCTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA
TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT
GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTGTATTAGCTACATTA
CCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG
AGGATATTAATTGTGATTTTATGTTTGTAACTTACAACTTTTCAAAGCATTAGTATGGT
CTGCTAGGTTGCAGGCTGTAGTTTACAAAACGAATATTGCAGTGAATATGTGATTCTTTAA
GGCTGCAATACAAGCATTAGTTCCTGTTTCAATAAGAGTCAATCCACATTACAAAGATG
CATTTTTTTCTTTTTTGATAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAATA
TAACACATATCTAGATTTTTCTGCTTGCATGATATTAGGTTTCAGGAATGAGCCTTGTAAT
ATAACTGGCTGTGCAGCTCTGCTTCTTTCTGTAAGTTTCAGCATGGGTGTGCCTTCATAC
AATAATATTTTTCTTTGTCTCCAACATAATAAAATGTTTTGCTAAATCTTACAATTTGA
AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC
TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT
AACTCAGTTCCTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATAACCATATGATTTT
TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCTTTTAAATGACAGCACA
GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAA
TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCCTATCACCTAATATTACAAGAGTTGGTA
AGCGCTCATCATTATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGGTATGGA
TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC
AGGAGGAAATTACAGAGACAATTATGACAACTGAAATGAGACATGCACATAATATAGATACA
CAAGGAATAATTTCTGATCCAGGATCGTCCTTCCAAATGGCTGTATTTATAAAGGTTTTTGG
AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATTGACCTGCCA
AGGTAGCTGAAGACCTTTTAGACAGTTCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA
AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 230

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGDTAVLR CYLED
GASKGAWLNRRSSIIFAGGDKWSVDPRVSI STL NKR DYS LQIQNV DVTDDGPYTCSVQTQH TP
RTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL
NPPSTAQYGITGSADVLFSCWYLVLTLSSTTSIFYLKNAILO

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGTTCTCTTGAGGGGAGCATTTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGTCATCGAGGCTG
CAAGTCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAACTTCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCGGGACCACCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCAAAGGGGAACTGGAATAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGGGGCCTCCTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTTTCTTGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCCGGGCCCTCCTGGTGAGTGGGACACCCAGGTGC
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAGGTGAAAGAGGTGAAAACCTCAGTGTTCC
GTCAGGATTGTTCGGCAGTAGTAACCGAGGCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAATTTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTTCAGTGTCGGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGACCCGGAAACCTTTTCA
CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMMPGAPGPPGPPAEKGAKGAMGRD
GATGPSGPQGPVGKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE
KGDGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGAKGDQGPGLQGVPG
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGGQGRKGESGVPGPA
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKSSGEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGGCCAAACTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATTGAAGATCTTCATGTATTCTGGAGAACACCATTCCCTGATTTC
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

10424 3307001

[illegible]

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<subunit 1 of 1, 98 aa, 1 stop
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MKLMVLVFTIGLTL LLGVQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG
 KCGEMICHVNESTLL

Important features:

amino acids 1-20

amino acids 72-76

amino acids 63-71

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCGTGGTGGTTGGAGGGC
 GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG
 TGAATCTCCTTACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG
 CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGGGTGGTTTA
 TAAAATCCTCCAATGAAGCTACTAACATTACTCAAAGCATAATATGAAAGCATTTTTTGAT
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
 AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCATCCAGTGGAAGAATTTGGCC
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTACCCAAATAAGACTCATCCC
 AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTCTCTCCTC
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTAACTATGCACGAACTGAAGACTTCTTTAAA
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATTGCCAGATATGGGAAAGT
 TTTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
 CCGACCCTGCTGACTACTTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCTT
 GGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCTCTCACACC
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGAATTTGCAGAGGCTGTTGGTCTTCCAA
 GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC
 TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCTTACAATGTTGGACCTGG
 CTTTACTGGAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT
 TGTTCATGAAATTTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA
 GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
 ACTAAAAAAGTCTTCCCCAGAGTTCAGTGGCATGCCAGGATAAGCAAATTGGGATCTGG
 AAATGATTTTGGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA
 AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT
 GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG
 AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATTATG
 CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT
 TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA
 TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTTATTGATCCATTAGGGTTACCAGAC
 AGGCCTTTTTTATAGGCATGTCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC
 ATTCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCT
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT
 TTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGT
 TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVIRYGVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQRGNILNLNGAGDPLTPGYPANNEYAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTIRIYNVIGTLRGAVEPDRYV
ILGGRHDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQERGVAIYNADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYES
WTKKSPSPFEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSLFSVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713